

SEQUENCE LISTING

<110> Korneluk, Robert G.
Mackenzie, Alexander E.

Baird, Stephen
Liston, Peter

<120> MAMMALIAN IAP GENE FAMILY, PRIMERS,
PROBES, AND DETECTION METHODS

<130> 07891/003005

<150> 08/576,956
<151> 1995-12-22

<150> 08/511,485
<151> 1995-08-04

<160> 92

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 46
<212> PRT
<213> artificial sequence based on Homo sapiens, Mus musculus, Cydia pomonella, Orgyia pseudotsugata, and Drosophila melanogaster.

<220>
<221> VARIANT
<222> 8
<223> Glu or Asp

<221> VARIANT
<222> 14,22
<223> Val or Ile

<221> VARIANT
<222> (1)...(46)
<223> Xaa = Any Amino Acid

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Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Lys Xaa Cys Met
1 5 10 15
Xaa Xaa Xaa Xaa Xaa Xaa Phe Xaa Pro Cys Gly His Xaa Xaa Xaa
20 25 30
Cys Xaa Xaa Cys Ala Xaa Xaa Xaa Xaa Cys Pro Xaa Cys
35 40 45

<210> 2
<211> 68
<212> PRT
<213> artificial sequence based on Homo sapiens, Mus musculus, Cydia pomonella, Orgyia pseudotsugata, and Drosophila melanogaster.

<220>
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<222> 13,16,17
<223> any amino acid or absent

<221> VARIANT
<222> (1)...(68)
<223> Xaa = Any Amino Acid

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Xaa Xaa Xaa Xaa Leu Ala Xaa Ala Gly Phe Tyr Tyr Xaa Gly Xaa
20 25 30
Xaa Asp Xaa Val Xaa Cys Phe Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Trp 26/68
35 40 45
Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa His Xaa Xaa Xaa Xaa Pro Xaa
50 55 60
Cys Xaa Phe Val
65

<210> 3
<211> 2540
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
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<223> n = A,T,C, or G

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ttaaaaactt ttgctaattt tccaaagtggc agtcctgttt cagcatcaac actggcacgca 180
gcagggtttc tttatactgg tgaaggagat accgtgcggt gcttttagtt tcattgcagct 240
gtagatagat ggcaatatgg agactcagca gttggaagac acaggaaagt atccccaaat 300
tgcagattta tcaacggctt ttatcttggaa aatagtgcac cgcatctac aaattctgg 360
atccagaatg gtcagttaca agttgaaaac tatctggaa gcagagatca ttttgcctta 420
gacaggccat ctgagacaca tgcagactat cttttgagaa ctgggcaggt tgttagatata 480
tcagacacca tatacccgag gaaccctgcc atgtattgtg aagaagctag attaaagtcc 540
tttcagaact ggccagacta tgctcaccta accccaagag agtttagcaag tgctggactc 600
tactacacag gtattggta ccaagtgcag tgctttgtt gtggtgaaa actgaaaaat 660
tggAACCTT gtgatcgtgc ctggcagaa cacaggcgac actttcctaa ttgcttcttt 720
gttttggcc ggaatcttaa tattcgaagt gaatctgatg ctgtgagttc tgataggaat 780
ttcccaaatt caacaaatct tccaagaaat ccatccatgg cagattatga agcacggatc 840

tttactttg ggacatggat atactcagtt aacaaggagc agcttgcaag agctggattt 900
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 tggaaagccca gtgaagaccc ttgggaacaa catgcataat ggtatccagg gtgcaaataat 1020
 ctgttagaac agaagggaca agaatatata aacaatattc attaactca ttcacttgag 1080
 gagtgctgg taagaactac tgagaaaaca ccatcactaa ctagaagaat tgatgatacc 1140
 atcttccaaa atcctatggt acaagaagct atacgaatgg gggttcagtt caaggacatt 1200
 aagaaaataa tggaggaaaa aattcagata tctggagca actataaaatc acttgaggtt 1260
 ctggttcag atcttagtcaa tgctcagaaa gacagtatgc aagatgagtc aagtcaact 1320
 tcattacaga aagagattag tactgaagag cagctaaaggc gcctgcaaga ggagaagctt 1380
 tgcaaaaatct gtatggatag aaatattgtt atcggttttgc ttccttgc acatctagtc 1440
 acttgtaaac aatgtgctga agcagttgac aagtgtccca tgtgctcacac agtcaattact 1500
 ttcaagcaaa aaattttat gtcttaatct aactctatag taggcattgtt atgttgc 1560
 tattaccctg attgaatgtg tgatgtgaac tgactttaag taatcaggat tgaattccat 1620
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 attcatagta tactgattt atttctaagt gtaagtgaat taatcatctg gattttttat 1860
 tctttcaga taggcttaac aaatggagct ttctgtatataatgtggag attagagttt 1920
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 gaaagataga gattgtttt agaggttggg tggtgttt taggattctg tccattttct 2040
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 gagatatgtt aagtgtaaaa tgcaagtggc gggacactat gtatagtctg agccagatca 2220
 aagtatgtat gttgttataa tgcatagaac gagagattt gaaagatata caccAAactg 2280
 ttaaatgtgg tttctcttcg gggagggggg gattggggga gggggcccccag aggggtttta 2340
 gaggggcctt ttcactttcg actttttca ttttgc ttcggatttt ttataagtat 2400
 gtagaccccg aagggtttta tgggaactaa catcagaac ctaacccccc tgactatcct 2460
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 ctgagtgcgtg gggcactttt 2540

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 <211> 497
 <212> PRT
 <213> Homo sapiens

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 Phe Ala Asn Phe Pro Ser Gly Ser Pro Val Ser Ala Ser Thr Leu Ala
 35 40 45
 Arg Ala Gly Phe Leu Tyr Thr Gly Glu Gly Asp Thr Val Arg Cys Phe
 50 55 60
 Ser Cys His Ala Ala Val Asp Arg Trp Gln Tyr Gly Asp Ser Ala Val
 65 70 75 80
 Gly Arg His Arg Lys Val Ser Pro Asn Cys Arg Phe Ile Asn Gly Phe
 85 90 95
 Tyr Leu Glu Asn Ser Ala Thr Gln Ser Thr Asn Ser Gly Ile Gln Asn
 100 105 110
 Gly Gln Tyr Lys Val Glu Asn Tyr Leu Gly Ser Arg Asp His Phe Ala
 115 120 125
 Leu Asp Arg Pro Ser Glu Thr His Ala Asp Tyr Leu Leu Arg Thr Gly
 130 135 140

Gln Val Val Asp Ile Ser Asp Thr Ile Tyr Pro Arg Asn Pro Ala Met
 145 150 155 160
 Tyr Cys Glu Glu Ala Arg Leu Lys Ser Phe Gln Asn Trp Pro Asp Tyr
 165 170 175
Ala His Leu Thr Pro Arg Glu Leu Ala Ser Ala Gly Leu Tyr Tyr Thr
 180 185 190
 Gly Ile Gly Asp Gln Val Gln Cys Phe Cys Cys Gly Gly Lys Leu Lys
 195 200 205
 Asn Trp Glu Pro Cys Asp Arg Ala Trp Ser Glu His Arg Arg His Phe
 210 215 220
 Pro Asn Cys Phe Phe Val Leu Gly Arg Asn Leu Asn Ile Arg Ser Glu
 225 230 235 240
 Ser Asp Ala Val Ser Ser Asp Arg Asn Phe Pro Asn Ser Thr Asn Leu
 245 250 255
 Pro Arg Asn Pro Ser Met Ala Asp Tyr Glu Ala Arg Ile Phe Thr Phe
 260 265 270
 Gly Thr Trp Ile Tyr Ser Val Asn Lys Glu Gln Leu Ala Arg Ala Gly
 275 280 285
 Phe Tyr Ala Leu Gly Glu Gly Asp Lys Val Lys Cys Phe His Cys Gly
 290 295 300
 Gly Gly Leu Thr Asp Trp Lys Pro Ser Glu Asp Pro Trp Glu Gln His
 305 310 315 320
 Ala Lys Trp Tyr Pro Gly Cys Lys Tyr Leu Leu Glu Gln Lys Gly Gln
 325 330 335
 Glu Tyr Ile Asn Asn Ile His Leu Thr His Ser Leu Glu Glu Cys Leu
 340 345 350
 Val Arg Thr Thr Glu Lys Thr Pro Ser Leu Thr Arg Arg Ile Asp Asp
 355 360 365
 Thr Ile Phe Gln Asn Pro Met Val Gln Glu Ala Ile Arg Met Gly Phe
 370 375 380
 Ser Phe Lys Asp Ile Lys Lys Ile Met Glu Glu Lys Ile Gln Ile Ser
 385 390 395 400
 Gly Ser Asn Tyr Lys Ser Leu Glu Val Leu Val Ala Asp Leu Val Asn
 405 410 415
 Ala Gln Lys Asp Ser Met Gln Asp Glu Ser Ser Gln Thr Ser Leu Gln
 420 425 430
 Lys Glu Ile Ser Thr Glu Glu Gln Leu Arg Arg Leu Gln Glu Glu Lys
 435 440 445
 Leu Cys Lys Ile Cys Met Asp Arg Asn Ile Ala Ile Val Phe Val Pro
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 Cys Gly His Leu Val Thr Cys Lys Gln Cys Ala Glu Ala Val Asp Lys
 465 470 475 480
 Cys Pro Met Cys Tyr Thr Val Ile Thr Phe Lys Gln Lys Ile Phe Met
 485 490 495
 Ser

<210> 5
 <211> 2676
 <212> DNA
 <213> Homo sapiens

<220>
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gcaaagccat gcacaaaact acctccctag agaaaggcta gtcctttc ttccccattc 180
atttcattat gaacatagta gaaaacagca tattttatc aaatttgatg aaaagcgcca 240
acacgttga actgaaatac gacttgtcat gtgactgtc ccgaatgtct acgtattcca 300
ctttccctgc tggggttcct gtctcagaaa ggagtcctgc tcgtgctggt ttcttattaca 360
ctgggtgaa tgacaaggc 420
gaggagacag tcctactgaa aagcataaaa agttgtatcc tagctgcaga ttcgttcaga 480
gtctaaattc cgtaacaac ttggaagcta cctctcagcc tactttcct tcttcagtaa 540
cacattccac acactcatta cttccggta cagaaaacag tggatatttc cgtggctt 600
attcaaactc tccatcaaat cctgtaaact ccagagcaaa tcaagaattt tctgccttga 660
tgagaagttc ctaccctgt ccaatgaata acgaaaatgc cagattactt actttcaga 720
catggccatt gactttctg tcgccaacag atctggcacg agcaggctt tactacatag 780
gacctggaga cagagtggct tgcttgcct gtgggtggaa attgagcaat tgggaaccga 840
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gactcaggtg ttggaatct ggagatgatc catgggttca acatgc当地 1140
ggtgtgagta cttgataaga attaaaggac aggagttcat cctgtcaagtt caagccagtt 1200
accctcatct acttgaacag ctgctatcca catcagacag cccaggagat gaaaatgcag 1260
agtcatcaat tatccatttgc aacactggag aagaccattc agaagatgca atcatgatga 1320
atactcctgt gattaatgtc gccgtggaaa tgggtttag tagaaggctg gtaaaacaga 1380
cagttcagag aaaaatccta gcaactggag agaattatag actagtcaat gatcttgcgt 1440
tagacttact caatgc当地 1500
aaaaagaatc aaatgatttt ttattatcc ggaagaatag aatggcactt tttcaacatt 1560
tgacttgcgtt aattccaatc ctggatagtc tactaactgc cggatttattt aatgaacaag 1620
aacatgtgtt tattaaacag aagacacaga cgtcttaca agcaagagaa ctgattgata 1680
cgattttgtt aaaaggaaat attgcagcca ctgttattcag aaactctctg caagaagctg 1740
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atgttcaga tctaccagtg gaagaacaat tgcggagact accagaagaa agaacatgt 1860
aagtgtgtat ggacaaagaa gtgtccatag tttttattcc ttgtggcat cttagtagtat 1920
gcaaagattt tgctccctt ttaagaaagt gtccttattt taggagtaca atcaagggtt 1980
cagttcgtac atttcttca tgaagaagaa ccaaaacatc gtctaaactt tagaattat 2040
ttattaaatg tattataact ttaacttttca tttttttttt aatttttattt 2100
tatttacaac tcaaaaaaca ttgtttgtt taacatattt atatatgtat ctaaaccata 2160
tgaacatata ttttttagaa actaagagaa tgataggctt ttgttctttagt 2220
gaggtagcac tacaacaca atattcaatc caaatttgc cattattgaa attgttaatg 2280
aagtaaaact taagatattt gagttaccc ttaagaattt taaatattt ggcattgtac 2340
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agagaattac ttgagcccgag gagtttgcattt ccatttttttccca ggctgaggca 2460
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cagtgtccta tacatcgaag gtgtgcataat atgttgaatc acatttttagg gacatgggtt 2580
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aaaaaaaaaaaa aaaaaactcg agggcccg accaat 2676

<210> 6
<211> 604
<212> PRT
<213> Homo sapiens

<400> 6
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20 25 30
Met Ser Thr Tyr Ser Thr Phe Pro Ala Gly Val Pro Val Ser Glu Arg
35 40 45
Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val Asn Asp Lys Val
50 55 60
Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp Lys Arg Gly Asp
65 70 75 80
Ser Pro Thr Glu Lys His Lys Leu Tyr Pro Ser Cys Arg Phe Val
85 90 95
Gln Ser Leu Asn Ser Val Asn Asn Leu Glu Ala Thr Ser Gln Pro Thr
100 105 110
Phe Pro Ser Ser Val Thr His Ser Thr His Ser Leu Leu Pro Gly Thr
115 120 125
Glu Asn Ser Gly Tyr Phe Arg Gly Ser Tyr Ser Asn Ser Pro Ser Asn
130 135 140
Pro Val Asn Ser Arg Ala Asn Gln Glu Phe Ser Ala Leu Met Arg Ser
145 150 155 160
Ser Tyr Pro Cys Pro Met Asn Asn Glu Asn Ala Arg Leu Leu Thr Phe
165 170 175
Gln Thr Trp Pro Leu Thr Phe Leu Ser Pro Thr Asp Leu Ala Arg Ala
180 185 190
Gly Phe Tyr Tyr Ile Gly Pro Gly Asp Arg Val Ala Cys Phe Ala Cys
195 200 205
Gly Gly Lys Leu Ser Asn Trp Glu Pro Lys Asp Asn Ala Met Ser Glu
210 215 220
His Leu Arg His Phe Pro Lys Cys Pro Phe Ile Glu Asn Gln Leu Gln
225 230 235 240
Asp Thr Ser Arg Tyr Thr Val Ser Asn Leu Ser Met Gln Thr His Ala
245 250 255
Ala Arg Phe Lys Thr Phe Phe Asn Trp Pro Ser Ser Val Leu Val Asn
260 265 270
Pro Glu Gln Leu Ala Ser Ala Gly Phe Tyr Tyr Val Gly Asn Ser Asp
275 280 285
Asp Val Lys Cys Phe Cys Cys Asp Gly Gly Leu Arg Cys Trp Glu Ser
290 295 300
Gly Asp Asp Pro Trp Val Gln His Ala Lys Trp Phe Pro Arg Cys Glu
305 310 315 320
Tyr Leu Ile Arg Ile Lys Gly Gln Glu Phe Ile Arg Gln Val Gln Ala
325 330 335
Ser Tyr Pro His Leu Leu Glu Gln Leu Leu Ser Thr Ser Asp Ser Pro
340 345 350
Gly Asp Glu Asn Ala Glu Ser Ser Ile Ile His Leu Glu Pro Gly Glu
355 360 365

Asp	His	Ser	Glu	Asp	Ala	Ile	Met	Met	Asn	Thr	Pro	Val	Ile	Asn	Ala
370			375						380						
Ala	Val	Glu	Met	Gly	Phe	Ser	Arg	Ser	Leu	Val	Lys	Gln	Thr	Val	Gln
385		390							395					400	
Arg	Lys	Ile	Leu	Ala	Thr	Gly	Glu	Asn	Tyr	Arg	Leu	Val	Asn	Asp	Leu
		405							410				415		
Val	Leu	Asp	Leu	Leu	Asn	Ala	Glu	Asp	Glu	Ile	Arg	Glu	Glu	Arg	
		420						425				430			
Glu	Arg	Ala	Thr	Glu	Glu	Lys	Glu	Ser	Asn	Asp	Leu	Leu	Ile	Arg	
		435					440				445				
Lys	Asn	Arg	Met	Ala	Leu	Phe	Gln	His	Leu	Thr	Cys	Val	Ile	Pro	Ile
		450				455				460					
Leu	Asp	Ser	Leu	Leu	Thr	Ala	Gly	Ile	Ile	Asn	Glu	Gln	Glu	His	Asp
		465				470				475			480		
Val	Ile	Lys	Gln	Lys	Thr	Gln	Thr	Ser	Leu	Gln	Ala	Arg	Glu	Leu	Ile
						485			490			495			
Asp	Thr	Ile	Leu	Val	Lys	Gly	Asn	Ile	Ala	Ala	Thr	Val	Phe	Arg	Asn
						500			505			510			
Ser	Leu	Gln	Glu	Ala	Glu	Ala	Val	Leu	Tyr	Glu	His	Leu	Phe	Val	Gln
						515			520			525			
Gln	Asp	Ile	Lys	Tyr	Ile	Pro	Thr	Glu	Asp	Val	Ser	Asp	Leu	Pro	Val
						530			535			540			
Glu	Glu	Gln	Leu	Arg	Arg	Leu	Pro	Glu	Glu	Arg	Thr	Cys	Lys	Val	Cys
						545			550			555			560
Met	Asp	Lys	Glu	Val	Ser	Ile	Val	Phe	Ile	Pro	Cys	Gly	His	Leu	Val
						565			570			575			
Val	Cys	Lys	Asp	Cys	Ala	Pro	Ser	Leu	Arg	Lys	Cys	Pro	Ile	Cys	Arg
						580			585			590			
Ser	Thr	Ile	Lys	Gly	Thr	Val	Arg	Thr	Phe	Leu	Ser				
						595			600						

<210> 7
<211> 2580
<212> DNA
<213> Homo sapiens

<220>
<221> Variant
<222> (1)...(2580)
<223> n = A,T,C,or G

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tgttagtaaat tctacataag agtcttatcat tgatttctt ttgtggtgaa aatcttagtt 180
catgtgaaga aatttcatgt gaatgtttt gctatcaaac agtactgtca cctactcatg 240
cacaaaactg cctcccaaag acttttccc ggtccctcgat atcaaaacat taagagtata 300
atggaagata gcacgatctt gtcagattgg acaaacacagca acaaacaaaa aatgaagtat 360
gactttccct gtgaactcta cagaatgtct acatattcaa ctttccccgc cgggggtgcct 420
gtctcagaaa ggagtcttgc tcgtgctgggt ttttattata ctgggtgtgaa tgacaaggtc 480
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aagcataaac agctatatcc tagctgttagc tttatttcaga atctggtttc agctagtctg 600
ggatccaccc ctaagaatac gtctccaatg agaaacagtt ttgcacattc attatctccc 660

accttggAAC atagtagctt gttcagtggT tcttactcca gccttcctcc aaacccttt 720
 aattctAGAG cagttGAAGA catctttca tcgaggACTA accccTACAG ttatGCAATG 780
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 tcagaATTGG caagAGCTGG ttttattat ataggACCTG gagatAGGGT agcctgCTTT 900
 gcctgtGGTG ggaagCTAG taactGGGAA ccaaAGGATG atgctatGTC agaacACCGG 960
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 tcaaATCTGA gcatGCAGAC acatGCAGCT cgaatGAGAA catttatGTA ctggccatCT 1080
 agtGTTCCAG ttcAGCCTGA gcagCTTGCA aGTGCTGGTT ttTATTATGT gggtcgcaAT 1140
 gatGatGTCA aatGCTTGG ttGtgatGGT ggcttGAGGT gttggGAATC tggAGATGAT 1200
 ccatGGGTAG aacatGCCA gtggTTCCA aggtGTGAGT tcttgatacG aatgaaAGGC 1260
 caagAGTTG ttGatGAGAT tcaAGGTAGA tatCCTCATC ttctGAACA gctGTTGTCA 1320
 acttcAGATA ccactGGAGA agaaaATGCT gaccCACCAA ttattcATTt tggacCTGG 1380
 gaaAGTTCTT cagaAGATGC tGTCATGATG aataCACCTG tggTTAAATC tgcCTTGGAA 1440
 atgggCTTTA atagAGACCT ggtGAAACAA acagttCTAA gtaAAATCCT gacaACTGG 1500
 gagaACTATA aaACAGTTA tgatATTGtG tcAGCActTC ttaATGCTGA agatgaaaa 1560
 agagaAGAGG agaAGGAAA acaAGCTGAA gaaATGGCAT cAGATGATTt gtcattAAATT 1620
 cggAAGAACa gaatGGCTCT ctttcaacAA ttGACATGTG tgcttCCtAt cctggataAt 1680
 ctTTAAAGG ccaatGtaAt taataAAACAG gaACATGATA ttattAAACA AAAAACACAG 1740
 atacCTTAC aAGCGAGAGA actGATTGAT accATTGGG ttAAAGGAAA tgctGCGGCC 1800
 aacatCTTCA aaaACTGTCT aaaAGGAAAtt gactCTACAT tGtATAAGAA cttatttGtG 1860
 gataAGAAATA tgaAGTATAT tccaACAGAA gatGTTTCAG gtcTGTCACT ggaAGAACAA 1920
 ttGAGGAGGT tgcaAGAAGA acgaACTTGT aaAGTGTGTA tggacAAAGA agtttCTGTT 1980
 gtatttattc ctGtGGTCA tctGGTAGtA tgccAGGAAt gtGcccCTtC tctaAGGAAA 2040
 tgccCTAttt gcAGGGGTAt aatcaAGGGT actGTTcGtA catttCTCtC ttaAGGAAA 2100
 atagtCTATA tttaACCTG cataAAAGG tcttAAAt attGTTGAAc acttGAAGCC 2160
 atctAAAGTA AAAAGGGAAt tatGAGTTT tcaATTAGTA acattCATGt tctAGTCTGc 2220
 ttGgtACTA ataAtCTTGT ttctGAAAAG atGGTATCAT atAttTAATC ttaAtCTGTT 2280
 tatttacaAG ggaAGATTa tgTTGGTGA actatATTAG tatGtATGTG tacctaAGGG 2340
 agtagCGTCN ctGCTTGTtA tgcatCATT caggAGTTAC tggatttGTT gttcttCAG 2400
 aaAGCTTGA anactAAAtt atAGTGTAGA aaAGAACTGG aaACCAGGAA ctctGGAGTT 2460
 catcAGAGTT atGGTGCCGA attGtCTTTG gtGctttCA cttGtGTTT AAAATAAGGA 2520
 ttttCTCTt atttCTCCCC ctGtttGtG agaaACATCT caAtAAAGtG cttaAAAGA 2580

<210> 8
 <211> 618
 <212> PRT
 <213> Homo sapiens

<400> 8
 Met His Lys Thr Ala Ser Gln Arg Leu Phe Pro Gly Pro Ser Tyr Gln
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 Asn Ile Lys Ser Ile Met Glu Asp Ser Thr Ile Leu Ser Asp Trp Thr
 20 25 30
 Asn Ser Asn Lys Gln Lys Met Lys Tyr Asp Phe Ser Cys Glu Leu Tyr
 35 40 45
 Arg Met Ser Thr Tyr Ser Thr Phe Pro Ala Gly Val Pro Val Ser Glu
 50 55 60
 Arg Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val Asn Asp Lys
 65 70 75 80
 Val Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp Lys Leu Gly
 85 90 95
 Asp Ser Pro Ile Gln Lys His Lys Gln Leu Tyr Pro Ser Cys Ser Phe
 100 105 110

Ile	Gln	Asn	Leu	Val	Ser	Ala	Ser	Leu	Gly	Ser	Thr	Ser	Lys	Asn	Thr
115								120					125		
Ser	Pro	Met	Arg	Asn	Ser	Phe	Ala	His	Ser	Leu	Ser	Pro	Thr	Leu	Glu
130							135				140				
His	Ser	Ser	Leu	Phe	Ser	Gly	Ser	Tyr	Ser	Ser	Leu	Pro	Pro	Asn	Pro
145				150					155				160		
Leu	Asn	Ser	Arg	Ala	Val	Glu	Asp	Ile	Ser	Ser	Ser	Arg	Thr	Asn	Pro
					165				170				175		
Tyr	Ser	Tyr	Ala	Met	Ser	Thr	Glu	Glu	Ala	Arg	Phe	Leu	Thr	Tyr	His
				180			185			190					
Met	Trp	Pro	Leu	Thr	Phe	Leu	Ser	Pro	Ser	Glu	Leu	Ala	Arg	Ala	Gly
					195		200			205					
Phe	Tyr	Tyr	Ile	Gly	Pro	Gly	Asp	Arg	Val	Ala	Cys	Phe	Ala	Cys	Gly
			210			215			220						
Gly	Lys	Leu	Ser	Asn	Trp	Glu	Pro	Lys	Asp	Asp	Ala	Met	Ser	Glu	His
225					230			235				240			
Arg	Arg	His	Phe	Pro	Asn	Cys	Pro	Phe	Leu	Glu	Asn	Ser	Leu	Glu	Thr
					245			250			255				
Leu	Arg	Phe	Ser	Ile	Ser	Asn	Leu	Ser	Met	Gln	Thr	His	Ala	Ala	Arg
				260			265			270					
Met	Arg	Thr	Phe	Met	Tyr	Trp	Pro	Ser	Ser	Val	Pro	Val	Gln	Pro	Glu
				275			280			285					
Gln	Leu	Ala	Ser	Ala	Gly	Phe	Tyr	Tyr	Val	Gly	Arg	Asn	Asp	Asp	Val
				290		295			300						
Lys	Cys	Phe	Gly	Cys	Asp	Gly	Gly	Leu	Arg	Cys	Trp	Glu	Ser	Gly	Asp
305					310			315			320				
Asp	Pro	Trp	Val	Glu	His	Ala	Lys	Trp	Phe	Pro	Arg	Cys	Glu	Phe	Leu
					325			330			335				
Ile	Arg	Met	Lys	Gly	Gln	Glu	Phe	Val	Asp	Glu	Ile	Gln	Gly	Arg	Tyr
					340			345			350				
Pro	His	Leu	Leu	Glu	Gln	Leu	Leu	Ser	Thr	Ser	Asp	Thr	Thr	Gly	Glu
					355			360			365				
Glu	Asn	Ala	Asp	Pro	Pro	Ile	Ile	His	Phe	Gly	Pro	Gly	Glu	Ser	Ser
					370			375			380				
Ser	Glu	Asp	Ala	Val	Met	Asn	Thr	Pro	Val	Val	Lys	Ser	Ala	Leu	
385					390			395			400				
Glu	Met	Gly	Phe	Asn	Arg	Asp	Leu	Val	Lys	Gln	Thr	Val	Leu	Ser	Lys
					405			410			415				
Ile	Leu	Thr	Thr	Gly	Glu	Asn	Tyr	Lys	Thr	Val	Asn	Asp	Ile	Val	Ser
					420			425			430				
Ala	Leu	Leu	Asn	Ala	Glu	Asp	Glu	Lys	Arg	Glu	Glu	Glu	Lys	Glu	Lys
					435			440			445				
Gln	Ala	Glu	Glu	Met	Ala	Ser	Asp	Asp	Leu	Ser	Ile	Arg	Lys	Asn	
					450			455			460				
Arg	Met	Ala	Leu	Phe	Gln	Gln	Leu	Thr	Cys	Val	Leu	Pro	Ile	Leu	Asp
465					470			475			480				
Asn	Leu	Leu	Lys	Ala	Asn	Val	Ile	Asn	Lys	Gln	Glu	His	Asp	Ile	Ile
					485			490			495				
Lys	Gln	Lys	Thr	Gln	Ile	Pro	Leu	Gln	Ala	Arg	Glu	Leu	Ile	Asp	Thr
					500			505			510				
Ile	Trp	Val	Lys	Gly	Asn	Ala	Ala	Asn	Ile	Phe	Lys	Asn	Cys	Leu	
					515			520			525				
Lys	Glu	Ile	Asp	Ser	Thr	Leu	Tyr	Lys	Asn	Leu	Phe	Val	Asp	Lys	Asn
					530			535			540				

Met	Lys	Tyr	Ile	Pro	Thr	Glu	Asp	Val	Ser	Gly	Leu	Ser	Leu	Glu	Glu
545						550				555				560	
Gln	Leu	Arg	Arg	Leu	Gln	Glu	Glu	Arg	Thr	Cys	Lys	Val	Cys	Met	Asp
						565			570				575		
Lys	Glu	Val	Ser	Val	Val	Phe	Ile	Pro	Cys	Gly	His	Leu	Val	Val	Cys
						580			585				590		
Gln	Glu	Cys	Ala	Pro	Ser	Leu	Arg	Lys	Cys	Pro	Ile	Cys	Arg	Gly	Ile
						595			600				605		
Ile	Lys	Gly	Thr	Val	Arg	Thr	Phe	Leu	Ser						
						610			615						

<210> 9
<211> 2100
<212> DNA
<213> Mus musculus

<400> 9
gacactctgc tggcgccgg gcccgcctcc tccgggacct cccctcgaaa accgtcgccc 60
gccccgccta gtttagactg gagtgcctgg cgcgaaaaagg tggacaagtc ctattttcca 120
gagaagatga cttaaacag ttttgaagga actagaactt ttgtacttgc agacaccaat 180
aaggatgaag aatttgtaga agagttaat agattaaaaa catttgctaa cttcccaagt 240
agttagcctg tttcagcatc aacattggcg cgagctgggt ttctttatac cggtaagga 300
gacaccgtgc aatgtttcag ttgtcatgcg gcaatagata gatggcagta tggagactca 360
gctgttggaa gacacaggag aatatccccca aattgcagat ttatcaatgg tttttatTTT 420
gaaaatggtg ctgcacagtc tacaaaatcccct ggtatccaaa atggccagta caaatctgaa 480
aactgtgtgg gaaatagaaaa tccttttgcg cctgacaggc cacctgagac tcatgctgat 540
tatctcttga gaactggaca ggttgttagat atttcagaca ccatatacc gaggaaccct 600
gccatgtgta gtgaagaagc cagattgaag tcatttcaga actggccggaa ctatgctcat 660
ttaaccccca gagagtttagc tagtgctggc ctctactaca caggggctga tgatcaagt 720
caatgctttt gttgtggggg aaaactgaaaa aattgggaac cctgtgatcg tgccctggta 780
gaacacagga gacactttcc caattgcTTT tttgtttgg gccggAACGT taatgttcga 840
agtgaatctg gtgtgagttc tgataggaat ttcccaaatt caacaaactc tccaaagaaaat 900
ccagccatgg cagaatatga agcacggatc gttacttttga acatggat atactcgtt 960
aacaaggagc agcttgcaag agctggattt tatgcTTT tagtgcggta taaagtgaag 1020
tgcttccact gtggaggagg gctcacggat tggaaGCCAA gtgaagaccc ctgggaccag 1080
catgctaagt gctacccagg gtgcaaatac ctattggatg agaaggggca agaatatata 1140
aataatattc atttaaccca tccacttgag gaatcttgg gaagaactgc tgaaaaaaca 1200
ccaccgctaa ctaaaaaaat cgatgatacc atcttccaga atcctatggt gcaagaagct 1260
atacgaatgg gatttagctt caaggacctt aagaaaaacaa tggaaaaaaa aatccaaaca 1320
tccgggagca gctatctatc acttgagggtc ctgattgcag atcttgcggat tgctcagaaa 1380
gataatacgg aggtgagtc aagtcaaact tcattgcaga aagacattag tactgaagag 1440
cagctaaggc gcctacaaga ggagaagctt tccaaaaatct gtatggatag aaatattgct 1500
atcgTTTTT ttccttgcgg acatctggcc acttgaaac agtgtgcaga agcagttgac 1560
aaatgtccca tgtgctacac cgtcattacg ttcaacccaaa aaatttttat gtcttagtgg 1620
ggcaccacat gttatgttct tttgcTTCTA attgaatgtg taatgggagc gaaaccttaag 1680
taatcctgca tttgcattcc attagcatcc tgctgtttcc aaatggagac caatgctaac 1740
agcactgttt ccgtctaaac attcaatttc tggatcttgc gatgtatcag ctgtatcatt 1800
tagccagtgt tttactcgat tggaaacccat gacagagaag cattttatag ctttcacat 1860
gtatattggt agtacactga ctgtatttct atatgtaaatgtaatgttcatca cctgcatttt 1920
tcatgcctt tgcataagct taacaaatgg agtgttctgt ataagcatgg agatgtgatg 1980
gaatctgccc aatgacttta attggcttatt tgtaaacacg gaaagaactg cccacgctg 2040
ctgggaggat aaagattgtt ttagatgctc acttgcgtt tttaggattc tgcccatTTA 2100

<210> 10
<211> 496
<212> PRT
<213> Homo sapiens

<400> 10
Met Thr Phe Asn Ser Phe Glu Gly Thr Arg Thr Phe Val Leu Ala Asp
1 5 10 15
Thr Asn Lys Asp Glu Glu Phe Val Glu Glu Phe Asn Arg Leu Lys Thr
20 25 30
Phe Ala Asn Phe Pro Ser Ser Pro Val Ser Ala Ser Thr Leu Ala
35 40 45
Arg Ala Gly Phe Leu Tyr Thr Gly Glu Gly Asp Thr Val Gln Cys Phe
50 55 60
Ser Cys His Ala Ala Ile Asp Arg Trp Gln Tyr Gly Asp Ser Ala Val
65 70 75 80
Gly Arg His Arg Arg Ile Ser Pro Asn Cys Arg Phe Ile Asn Gly Phe
85 90 95
Tyr Phe Glu Asn Gly Ala Ala Gln Ser Thr Asn Pro Gly Ile Gln Asn
100 105 110
Gly Gln Tyr Lys Ser Glu Asn Cys Val Gly Asn Arg Asn Pro Phe Ala
115 120 125
Pro Asp Arg Pro Pro Glu Thr His Ala Asp Tyr Leu Leu Arg Thr Gly
130 135 140
Gln Val Val Asp Ile Ser Asp Thr Ile Tyr Pro Arg Asn Pro Ala Met
145 150 155 160
Cys Ser Glu Glu Ala Arg Leu Lys Ser Phe Gln Asn Trp Pro Asp Tyr
165 170 175
Ala His Leu Thr Pro Arg Glu Leu Ala Ser Ala Gly Leu Tyr Tyr Thr
180 185 190
Gly Ala Asp Asp Gln Val Gln Cys Phe Cys Cys Gly Gly Lys Leu Lys
195 200 205
Asn Trp Glu Pro Cys Asp Arg Ala Trp Ser Glu His Arg Arg His Phe
210 215 220
Pro Asn Cys Phe Phe Val Leu Gly Arg Asn Val Asn Val Arg Ser Glu
225 230 235 240
Ser Gly Val Ser Ser Asp Arg Asn Phe Pro Asn Ser Thr Asn Ser Pro
245 250 255
Arg Asn Pro Ala Met Ala Glu Tyr Glu Ala Arg Ile Val Thr Phe Gly
260 265 270
Thr Trp Ile Tyr Ser Val Asn Lys Glu Gln Leu Ala Arg Ala Gly Phe
275 280 285
Tyr Ala Leu Gly Glu Gly Asp Lys Val Lys Cys Phe His Cys Gly Gly
290 295 300
Gly Leu Thr Asp Trp Lys Pro Ser Glu Asp Pro Trp Asp Gln His Ala
305 310 315 320
Lys Cys Tyr Pro Gly Cys Lys Tyr Leu Leu Asp Glu Lys Gly Gln Glu
325 330 335
Tyr Ile Asn Asn Ile His Leu Thr His Pro Leu Glu Glu Ser Leu Gly
340 345 350
Arg Thr Ala Glu Lys Thr Pro Pro Leu Thr Lys Lys Ile Asp Asp Thr
355 360 365
Ile Phe Gln Asn Pro Met Val Gln Glu Ala Ile Arg Met Gly Phe Ser
370 375 380

Phe	Lys	Asp	Leu	Lys	Lys	Thr	Met	Glu	Glu	Lys	Ile	Gln	Thr	Ser	Gly
385															400
Ser	Ser	Tyr	Leu	Ser	Leu	Glu	Val	Leu	Ile	Ala	Asp	Leu	Val	Ser	Ala
									405						415
Gln	<u>Lys</u>	<u>Asp</u>	<u>Asn</u>	<u>Thr</u>	<u>Glu</u>	<u>Asp</u>	<u>Glu</u>	<u>Ser</u>	<u>Ser</u>	<u>Gln</u>	<u>Thr</u>	<u>Ser</u>	<u>Leu</u>	<u>Gln</u>	<u>Lys</u>
									420						430
Asp	Ile	Ser	Thr	Glu	Glu	Gln	Leu	Arg	Arg	Leu	Gln	Glu	Glu	Lys	Leu
								435							445
Ser	Lys	Ile	Cys	Met	Asp	Arg	Asn	Ile	Ala	Ile	Val	Phe	Phe	Pro	Cys
								450				455			460
Gly	His	Leu	Ala	Thr	Cys	Lys	Gln	Cys	Ala	Glu	Ala	Val	Asp	Lys	Cys
								465				470			480
Pro	Met	Cys	Tyr	Thr	Val	Ile	Thr	Phe	Asn	Gln	Lys	Ile	Phe	Met	Ser
								485				490			495

<210> 11
<211> 67
<212> PRT
<213> Orgyia pseudotsugata

<400> 11															
Lys	Ala	Ala	Arg	Leu	Gly	Thr	Tyr	Thr	Asn	Trp	Pro	Val	Gln	Phe	Leu
1				5					10						15
Glu	Pro	Ser	Arg	Met	Ala	Ala	Ser	Gly	Phe	Tyr	Tyr	Leu	Gly	Arg	Gly
								20			25				30
Asp	Glu	Val	Arg	Cys	Ala	Phe	Cys	Lys	Val	Glu	Ile	Thr	Asn	Trp	Val
								35			40				45
Arg	Gly	Asp	Asp	Pro	Glu	Thr	Asp	His	Lys	Arg	Trp	Ala	Pro	Gln	Cys
								50			55				60
Pro	Phe	Val													
65															

<210> 12
<211> 275
<212> PRT
<213> Cydia pomonella

<400> 12															
Met	Ser	Asp	Leu	Arg	Leu	Glu	Glu	Val	Arg	Leu	Asn	Thr	Phe	Glu	Lys
1								5							15
Trp	Pro	Val	Ser	Phe	Leu	Ser	Pro	Glu	Thr	Met	Ala	Lys	Asn	Gly	Phe
								20			25				30
Tyr	Tyr	Leu	Gly	Arg	Ser	Asp	Glu	Val	Arg	Cys	Ala	Phe	Cys	Lys	Val
								35			40				45
Glu	Ile	Met	Arg	Trp	Lys	Glu	Gly	Glu	Asp	Pro	Ala	Ala	Asp	His	Lys
								50			55				60
Lys	Trp	Ala	Pro	Gln	Cys	Pro	Phe	Val	Lys	Gly	Ile	Asp	Val	Cys	Gly
								65			70				80
Ser	Ile	Val	Thr	Thr	Asn	Asn	Ile	Gln	Asn	Thr	Thr	Thr	His	Asp	Thr
								85			90				95
Ile	Ile	Gly	Pro	Ala	His	Pro	Lys	Tyr	Ala	His	Glu	Ala	Ala	Arg	Val
								100			105				110

Lys Ser Phe His Asn Trp Pro Arg Cys Met Gln Arg Pro Glu Gln
 115 120 125
 Met Ala Asp Ala Gly Phe Phe Tyr Thr Gly Tyr Gly Asp Asn Thr Lys
 130 135 140
Cys Phe Tyr Cys Asp Gly Gly Leu Lys Asp Trp Glu Pro Glu Asp Val
 145 150 155 160
 Pro Trp Glu Gln His Val Arg Trp Phe Asp Arg Cys Ala Tyr Val Gln
 165 170 175
 Leu Val Lys Gly Arg Asp Tyr Val Gln Lys Val Ile Thr Glu Ala Cys
 180 185 190
 Val Leu Pro Gly Glu Asn Thr Thr Val Ser Thr Ala Ala Pro Val Ser
 195 200 205
 Glu Pro Ile Pro Glu Thr Lys Ile Glu Lys Glu Pro Gln Val Glu Asp
 210 215 220
 Ser Lys Leu Cys Lys Ile Cys Tyr Val Glu Glu Cys Ile Val Cys Phe
 225 230 235 240
 Val Pro Cys Gly His Val Val Ala Cys Ala Lys Cys Ala Leu Ser Val
 245 250 255
 Asp Lys Cys Pro Met Cys Arg Lys Ile Val Thr Ser Val Leu Lys Val
 260 265 270
 Tyr Phe Ser
 275

<210> 13
 <211> 498
 <212> PRT
 <213> Drosophila melanogaster

<400> 13
 Met Thr Glu Leu Gly Met Glu Leu Glu Ser Val Arg Leu Ala Thr Phe
 1 5 10 15
 Gly Glu Trp Pro Leu Asn Ala Pro Val Ser Ala Glu Asp Leu Val Ala
 20 25 30
 Asn Gly Phe Phe Ala Thr Gly Lys Trp Leu Glu Ala Glu Cys His Phe
 35 40 45
 Cys His Val Arg Ile Asp Arg Trp Glu Tyr Gly Asp Gln Val Ala Glu
 50 55 60
 Arg His Arg Arg Ser Ser Pro Ile Cys Ser Met Val Leu Ala Pro Asn
 65 70 75 80
 His Cys Gly Asn Val Pro Arg Ser Gln Glu Ser Asp Asn Glu Gly Asn
 85 90 95
 Ser Val Val Asp Ser Pro Glu Ser Cys Ser Cys Pro Asp Leu Leu Leu
 100 105 110
 Glu Ala Asn Arg Leu Val Thr Phe Lys Asp Trp Pro Asn Pro Asn Ile
 115 120 125
 Thr Pro Gln Ala Leu Ala Lys Ala Gly Phe Tyr Tyr Leu Asn Arg Leu
 130 135 140
 Asp His Val Lys Cys Val Trp Cys Asn Gly Val Ile Ala Lys Trp Glu
 145 150 155 160
 Lys Asn Asp Asn Ala Phe Glu Glu His Lys Arg Phe Phe Pro Gln Cys
 165 170 175
 Pro Arg Val Gln Met Gly Pro Leu Ile Glu Phe Ala Thr Gly Lys Asn
 180 185 190

Leu	Asp	Glu	Leu	Gly	Ile	Gln	Pro	Thr	Thr	Leu	Pro	Leu	Arg	Pro	Lys
195							200					205			
Tyr	Ala	Cys	Val	Asp	Ala	Arg	Leu	Arg	Thr	Phe	Thr	Asp	Trp	Pro	Ile
210							215					220			
Ser	Asn	Ile	Gln	Pro	Ala	Ser	Ala	Leu	Ala	Gln	Ala	Gly	Leu	Tyr	Tyr
225							230				235			240	
Gln	Lys	Ile	Gly	Asp	Gln	Val	Arg	Cys	Phe	His	Cys	Asn	Ile	Gly	Leu
							245			250			255		
Arg	Ser	Trp	Gln	Lys	Glu	Asp	Glu	Pro	Trp	Phe	Glu	His	Ala	Lys	Trp
							260			265			270		
Ser	Pro	Lys	Cys	Gln	Phe	Val	Leu	Leu	Ala	Lys	Gly	Pro	Ala	Tyr	Val
							275			280			285		
Ser	Glu	Val	Leu	Ala	Thr	Thr	Ala	Ala	Asn	Ala	Ser	Ser	Gln	Pro	Ala
							290			295			300		
Thr	Ala	Pro	Ala	Pro	Thr	Leu	Gln	Ala	Asp	Val	Leu	Met	Asp	Glu	Ala
305							310				315			320	
Pro	Ala	Lys	Glu	Ala	Leu	Thr	Leu	Gly	Ile	Asp	Gly	Gly	Val	Val	Arg
							325			330			335		
Asn	Ala	Ile	Gln	Arg	Lys	Leu	Leu	Ser	Ser	Gly	Cys	Ala	Phe	Ser	Thr
							340			345			350		
Leu	Asp	Glu	Leu	Leu	His	Asp	Ile	Phe	Asp	Asp	Ala	Gly	Ala	Gly	Ala
							355			360			365		
Ala	Leu	Glu	Val	Arg	Glu	Pro	Pro	Glu	Pro	Ser	Ala	Pro	Phe	Ile	Glu
							370			375			380		
Pro	Cys	Gln	Ala	Thr	Thr	Ser	Lys	Ala	Ala	Ser	Val	Pro	Ile	Pro	Val
385							390				395			400	
Ala	Asp	Ser	Ile	Pro	Ala	Lys	Pro	Gln	Ala	Ala	Glu	Ala	Val	Ser	Asn
							405				410			415	
Ile	Ser	Lys	Ile	Thr	Asp	Glu	Ile	Gln	Lys	Met	Ser	Val	Ser	Thr	Pro
							420			425			430		
Asn	Gly	Asn	Leu	Ser	Leu	Glu	Glu	Asn	Arg	Gln	Leu	Lys	Asp	Ala	
							435			440			445		
Arg	Leu	Cys	Lys	Val	Cys	Leu	Asp	Glu	Glu	Val	Gly	Val	Val	Phe	Leu
							450			455			460		
Pro	Cys	Gly	His	Leu	Ala	Thr	Cys	Asn	Gln	Cys	Ala	Pro	Ser	Val	Ala
465							470				475			480	
Asn	Cys	Pro	Met	Cys	Arg	Ala	Asp	Ile	Lys	Gly	Phe	Val	Arg	Thr	Phe
							485			490			495		
Leu	Ser														

<210> 14
<211> 67
<212> PRT
<213> Cydia pomonella

<400> 14
Glu Glu Val Arg Leu Asn Thr Phe Glu Lys Trp Pro Val Ser Phe Leu
1 5 10 15
Ser Pro Glu Thr Met Ala Lys Asn Gly Phe Tyr Tyr Leu Gly Arg Ser
20 25 30
Asp Glu Val Arg Cys Ala Phe Cys Lys Val Glu Ile Met Arg Trp Lys
35 40 45

Glu Gly Glu Asp Pro Ala Ala Asp His Lys Lys Trp Ala Pro Gln Cys
50 55 60
Pro Phe Val
65

<210> 15
<211> 67
<212> PRT
<213> Homo sapiens

<400> 15
Glu Ala Asn Arg Leu Val Thr Phe Lys Asp Trp Pro Asn Pro Asn Ile
1 5 10 15
Thr Pro Gln Ala Leu Ala Lys Ala Gly Phe Tyr Tyr Leu Asn Arg Leu
20 25 30
Asp His Val Lys Cys Val Trp Cys Asn Gly Val Ile Ala Lys Trp Glu
35 40 45
Lys Asn Asp Asn Ala Phe Glu Glu His Lys Arg Phe Phe Pro Gln Cys
50 55 60
Pro Arg Val
65

<210> 16
<211> 68
<212> PRT
<213> Mus musculus

<400> 16
Glu Phe Asn Arg Leu Lys Thr Phe Ala Asn Phe Pro Ser Ser Ser Pro
1 5 10 15
Val Ser Ala Ser Thr Leu Ala Arg Ala Gly Phe Leu Tyr Thr Gly Glu
20 25 30
Gly Asp Thr Val Gln Cys Phe Ser Cys His Ala Ala Ile Asp Arg Trp
35 40 45
Gln Tyr Gly Asp Ser Ala Val Gly Arg His Arg Arg Ile Ser Pro Asn
50 55 60
Cys Arg Phe Ile
65

<210> 17
<211> 68
<212> PRT
<213> Homo sapiens

<400> 17
Glu Phe Asn Arg Leu Lys Thr Phe Ala Asn Phe Pro Ser Gly Ser Pro
1 5 10 15
Val Ser Ala Ser Thr Leu Ala Arg Ala Gly Phe Leu Tyr Thr Gly Glu
20 25 30
Gly Asp Thr Val Arg Cys Phe Ser Cys His Ala Ala Val Asp Arg Trp
35 40 45

Gln Tyr Gly Asp Ser Ala Val Gly Arg His Arg Lys Val Ser Pro Asn
50 55 60
Cys Arg Phe Ile
65

<210> 18
<211> 68
<212> PRT
<213> Homo sapiens

<400> 18
Glu Leu Tyr Arg Met Ser Thr Tyr Ser Thr Phe Pro Ala Gly Val Pro
1 5 10 15
Val Ser Glu Arg Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val
20 25 30
Asn Asp Lys Val Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp
35 40 45
Lys Arg Gly Asp Ser Pro Thr Glu Lys His Lys Lys Leu Tyr Pro Ser
50 55 60
Cys Arg Phe Val
65

<210> 19
<211> 68
<212> PRT
<213> Homo sapiens

<400> 19
Glu Leu Tyr Arg Met Ser Thr Tyr Ser Thr Phe Pro Ala Gly Val Pro
1 5 10 15
Val Ser Glu Arg Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val
20 25 30
Asn Asp Lys Val Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp
35 40 45
Lys Leu Gly Asp Ser Pro Ile Gln Lys His Lys Gln Leu Tyr Pro Ser
50 55 60
Cys Ser Phe Ile
65

<210> 20
<211> 68
<212> PRT
<213> Mus musculus

<400> 20
Glu Glu Ala Arg Leu Lys Ser Phe Gln Asn Trp Pro Asp Tyr Ala His
1 5 10 15
Leu Thr Pro Arg Glu Leu Ala Ser Ala Gly Leu Tyr Tyr Thr Gly Ala
20 25 30
Asp Asp Gln Val Gln Cys Phe Cys Cys Gly Gly Lys Leu Lys Asn Trp
35 40 45

Glu Pro Cys Asp Arg Ala Trp Ser Glu His Arg Arg His Phe Pro Asn
50 55 60
Cys Phe Phe Val
65

<210> 21
<211> 68
<212> PRT
<213> Homo sapiens

<400> 21
Glu Glu Ala Arg Leu Lys Ser Phe Gln Asn Trp Pro Asp Tyr Ala His
1 5 10 15
Leu Thr Pro Arg Glu Leu Ala Ser Ala Gly Leu Tyr Tyr Thr Gly Ile
20 25 30
Gly Asp Gln Val Gln Cys Phe Cys Cys Gly Gly Lys Leu Lys Asn Trp
35 40 45
Glu Pro Cys Asp Arg Ala Trp Ser Glu His Arg Arg His Phe Pro Asn
50 55 60
Cys Phe Phe Val
65

<210> 22
<211> 67
<212> PRT
<213> Homo sapiens

<400> 22
Glu Asn Ala Arg Leu Leu Thr Phe Gln Thr Trp Pro Leu Thr Phe Leu
1 5 10 15
Ser Pro Thr Asp Leu Ala Arg Ala Gly Phe Tyr Tyr Ile Gly Pro Gly
20 25 30
Asp Arg Val Ala Cys Phe Ala Cys Gly Gly Lys Leu Ser Asn Trp Glu
35 40 45
Pro Lys Asp Asn Ala Met Ser Glu His Leu Arg His Phe Pro Lys Cys
50 55 60
Pro Phe Ile
65

<210> 23
<211> 67
<212> PRT
<213> Homo sapiens

<400> 23
Glu Glu Ala Arg Phe Leu Thr Tyr His Met Trp Pro Leu Thr Phe Leu
1 5 10 15
Ser Pro Ser Glu Leu Ala Arg Ala Gly Phe Tyr Tyr Ile Gly Pro Gly
20 25 30
Asp Arg Val Ala Cys Phe Ala Cys Gly Gly Lys Leu Ser Asn Trp Glu
35 40 45

Pro Lys Asp Asp Ala Met Ser Glu His Arg Arg His Phe Pro Asn Cys
50 55 60
Pro Phe Leu
65

<210> 24
<211> 66
<212> PRT
<213> Mus musculus

<400> 24
Tyr Glu Ala Arg Ile Val Thr Phe Gly Thr Trp Ile Tyr Ser Val Asn
1 5 10 15
Lys Glu Gln Leu Ala Arg Ala Gly Phe Tyr Ala Leu Gly Glu Gly Asp
20 25 30
Lys Val Lys Cys Phe His Cys Gly Gly Leu Thr Asp Trp Lys Pro
35 40 45
Ser Glu Asp Pro Trp Asp Gln His Ala Lys Cys Tyr Pro Gly Cys Lys
50 55 60
Tyr Leu
65

<210> 25
<211> 66
<212> PRT
<213> Homo sapiens

<400> 25
Tyr Glu Ala Arg Ile Phe Thr Phe Gly Thr Trp Ile Tyr Ser Val Asn
1 5 10 15
Lys Glu Gln Leu Ala Arg Ala Gly Phe Tyr Ala Leu Gly Glu Gly Asp
20 25 30
Lys Val Lys Cys Phe His Cys Gly Gly Leu Thr Asp Trp Lys Pro
35 40 45
Ser Glu Asp Pro Trp Glu Gln His Ala Lys Trp Tyr Pro Gly Cys Lys
50 55 60
Tyr Leu
65

<210> 26
<211> 68
<212> PRT
<213> Homo sapiens

<400> 26
His Ala Ala Arg Phe Lys Thr Phe Phe Asn Trp Pro Ser Ser Val Leu
1 5 10 15
Val Asn Pro Glu Gln Leu Ala Ser Ala Gly Phe Tyr Tyr Val Gly Asn
20 25 30
Ser Asp Asp Val Lys Cys Phe Cys Cys Asp Gly Gly Leu Arg Cys Trp
35 40 45

Glu Ser Gly Asp Asp Pro Trp Val Gln His Ala Lys Trp Phe Pro Arg
50 55 60
Cys Glu Tyr Leu
65

<210> 27
<211> 68
<212> PRT
<213> Homo sapiens

<400> 27
His Ala Ala Arg Met Arg Thr Phe Met Tyr Trp Pro Ser Ser Val Pro
1 5 10 15
Val Gln Pro Glu Gln Leu Ala Ser Ala Gly Phe Tyr Tyr Val Gly Arg
20 25 30
Asn Asp Asp Val Lys Cys Phe Gly Cys Asp Gly Gly Leu Arg Cys Trp
35 40 45
Glu Ser Gly Asp Asp Pro Trp Val Glu His Ala Lys Trp Phe Pro Arg
50 55 60
Cys Glu Phe Leu
65

<210> 28
<211> 68
<212> PRT
<213> Orgyia pseudotsugata

<400> 28
Glu Ala Ala Arg Leu Arg Thr Phe Ala Glu Trp Pro Arg Gly Leu Lys
1 5 10 15
Gln Arg Pro Glu Glu Leu Ala Glu Ala Gly Phe Phe Tyr Thr Gly Gln
20 25 30
Gly Asp Lys Thr Arg Cys Phe Cys Cys Asp Gly Gly Leu Lys Asp Trp
35 40 45
Glu Pro Asp Asp Ala Pro Trp Gln Gln His Ala Arg Trp Tyr Asp Arg
50 55 60
Cys Glu Tyr Val
65

<210> 29
<211> 68
<212> PRT
<213> Cydia pomonella

<400> 29
Glu Ala Ala Arg Val Lys Ser Phe His Asn Trp Pro Arg Cys Met Lys
1 5 10 15
Gln Arg Pro Glu Gln Met Ala Asp Ala Gly Phe Phe Tyr Thr Gly Tyr
20 25 30
Gly Asp Asn Thr Lys Cys Phe Tyr Cys Asp Gly Gly Leu Lys Asp Trp
35 40 45

Glu Pro Glu Asp Val Pro Trp Glu Gln His Val Arg Trp Phe Asp Arg
50 55 60
Cys Ala Tyr Val
65

<210> 30
<211> 68
<212> PRT
<213> Drosophila melanogaster

<400> 30
Val Asp Ala Arg Leu Arg Thr Phe Thr Asp Trp Pro Ile Ser Asn Ile
1 5 10 15
Gln Pro Ala Ser Ala Leu Ala Gln Ala Gly Leu Tyr Tyr Gln Lys Ile
20 25 30
Gly Asp Gln Val Arg Cys Phe His Cys Asn Ile Gly Leu Arg Ser Trp
35 40 45
Gln Lys Glu Asp Glu Pro Trp Phe Glu His Ala Lys Trp Ser Pro Lys
50 55 60
Cys Gln Phe Val
65

<210> 31
<211> 66
<212> PRT
<213> Drosophila melanogaster

<400> 31
Glu Ser Val Arg Leu Ala Thr Phe Gly Glu Trp Pro Leu Asn Ala Pro
1 5 10 15
Val Ser Ala Glu Asp Leu Val Ala Asn Gly Phe Phe Gly Thr Trp Met
20 25 30
Glu Ala Glu Cys Asp Phe Cys His Val Arg Ile Asp Arg Trp Glu Tyr
35 40 45
Gly Asp Leu Val Ala Glu Arg His Arg Arg Ser Ser Pro Ile Cys Ser
50 55 60
Met Val
65

<210> 32
<211> 46
<212> PRT
<213> Homo sapiens

<400> 32
Glu Gln Leu Arg Arg Leu Gln Glu Glu Arg Thr Cys Lys Val Cys Met
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Asp Lys Glu Val Ser Val Val Phe Ile Pro Cys Gly His Leu Val Val
20 25 30
Cys Gln Glu Cys Ala Pro Ser Leu Arg Lys Cys Pro Ile Cys
35 40 45

<210> 33
<211> 46
<212> PRT
<213> Homo sapiens

<400> 33
Glu Gln Leu Arg Arg Leu Pro Glu Glu Arg Thr Cys Lys Val Cys Met
1 5 10 15
Asp Lys Glu Val Ser Ile Val Phe Ile Pro Cys Gly His Leu Val Val
20 25 30
Cys Lys Asp Cys Ala Pro Ser Leu Arg Lys Cys Pro Ile Cys
35 40 45

<210> 34
<211> 46
<212> PRT
<213> Homo sapiens

<400> 34
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1 5 10 15
Asp Arg Asn Ile Ala Ile Val Phe Phe Pro Cys Gly His Leu Ala Thr
20 25 30
Cys Lys Gln Cys Ala Glu Ala Val Asp Lys Cys Pro Met Cys
35 40 45

<210> 35
<211> 46
<212> PRT
<213> Homo sapiens

<400> 35
Glu Gln Leu Arg Arg Leu Gln Glu Glu Lys Leu Cys Lys Ile Cys Met
1 5 10 15
Asp Arg Asn Ile Ala Ile Val Phe Val Pro Cys Gly His Leu Val Thr
20 25 30
Cys Lys Gln Cys Ala Glu Ala Val Asp Lys Cys Pro Met Cys
35 40 45

<210> 36
<211> 46
<212> PRT
<213> Drosophila melanogaster

<400> 36
Glu Glu Asn Arg Gln Leu Lys Asp Ala Arg Leu Cys Lys Val Cys Leu
1 5 10 15
Asp Glu Glu Val Gly Val Val Phe Leu Pro Cys Gly His Leu Ala Thr
20 25 30
Cys Asn Gln Cys Ala Pro Ser Val Ala Asn Cys Pro Met Cys
35 40 45

<210> 37
<211> 46
<212> PRT
<213> Cydia pomonella

<400> 37
Glu Lys Glu Pro Gln Val Glu Asp Ser Lys Leu Cys Lys Ile Cys Tyr
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Val Glu Glu Cys Ile Val Cys Phe Val Pro Cys Gly His Val Val Ala
20 25 30
Cys Ala Lys Cys Ala Leu Ser Val Asp Lys Cys Pro Met Cys
35 40 45

<210> 38
<211> 46
<212> PRT
<213> Orgyia pseudotsugata

<400> 38
Ala Val Glu Ala Glu Val Ala Asp Asp Arg Leu Cys Lys Ile Cys Leu
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Gly Ala Glu Lys Thr Val Cys Phe Val Pro Cys Gly His Val Val Ala
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Cys Gly Lys Cys Ala Ala Gly Val Thr Thr Cys Pro Val Cys
35 40 45

<210> 39
<211> 2474
<212> DNA
<213> Mus musculus

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atccccagag aaagacttgt ccctccccct ccctgtcatc tcaccatgaa catggttcaa 180
gacagcgcct ttcttagccaa gctgatgaag agtgctgaca ctttgagtt gaagtatgac 240
tttcctgtg agctgtaccc attgtccacg tattcagctt ttcccagggg agttcctgtg 300

tcagaaagga gtctggctcg tgctggctt tactacactg gtgccaatga caaggtcaag 360
 tgcttcgtct gttgcctgat gctagacaac tggaaacaag gggacagtcc catggagaag 420
 cacagaaagt tgtaccccag ctgcaacttt gtacagactt tgaatccagc caacagtctg 480
 gaagctagtc ctcggccttc tcttccttcc acggcgatga gcaccatgcc tttgagctt 540
gcaagttctg_agaatactgg ctatccagt_ggcttact cgagcttcc ctcagaccct 600
 gtgaacttcc gagcaaatca agattgtccct gctttgagca caagtcccta ccactttgca 660
 atgaacacag agaaggccag attactcacc tatgaaaacat ggccattgtc ttttctgtca 720
 ccagcaaagc tggccaaagc aggcttctac tacataggac ctggagatag agtggcctgc 780
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 cagaggcatt tccccagctg tccgttctta aaagacttgg gtcagtctgc ttcgagatac 900
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 ctaatggtcc atggctgcaa cttcagccag gaggaagttc actgtcactc ccagttccat 2040
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<210> 40
 <211> 602
 <212> PRT
 <213> Mus musculus

<400> 40
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 Leu Ser Thr Tyr Ser Ala Phe Pro Arg Gly Val Pro Val Ser Glu Arg
 35 40 45
 Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Ala Asn Asp Lys Val
 50 55 60
 Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp Lys Gln Gly Asp
 65 70 75 80

Ser	Pro	Met	Glu	Lys	His	Arg	Lys	Leu	Tyr	Pro	Ser	Cys	Asn	Phe	Val
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Gln	Thr	Leu	Asn	Pro	Ala	Asn	Ser	Leu	Glu	Ala	Ser	Pro	Arg	Pro	Ser
			100					105					110		
Leu	Pro	Ser	Thr	Ala	Met	Ser	Thr	Met	Pro	Leu	Ser	Phe	Ala	Ser	Ser
			115					120				125			
Glu	Asn	Thr	Gly	Tyr	Phe	Ser	Gly	Ser	Tyr	Ser	Ser	Phe	Pro	Ser	Asp
			130				135					140			
Pro	Val	Asn	Phe	Arg	Ala	Asn	Gln	Asp	Cys	Pro	Ala	Leu	Ser	Thr	Ser
			145				150		155				160		
Pro	Tyr	His	Phe	Ala	Met	Asn	Thr	Glu	Lys	Ala	Arg	Leu	Leu	Thr	Tyr
			165					170				175			
Glu	Thr	Trp	Pro	Leu	Ser	Phe	Leu	Ser	Pro	Ala	Lys	Leu	Ala	Lys	Ala
			180					185				190			
Gly	Phe	Tyr	Tyr	Ile	Gly	Pro	Gly	Asp	Arg	Val	Ala	Cys	Phe	Ala	Cys
			195				200				205				
Asp	Gly	Lys	Leu	Ser	Asn	Trp	Glu	Arg	Lys	Asp	Asp	Ala	Met	Ser	Glu
			210				215				220				
His	Gln	Arg	His	Phe	Pro	Ser	Cys	Pro	Phe	Leu	Lys	Asp	Leu	Gly	Gln
			225				230			235			240		
Ser	Ala	Ser	Arg	Tyr	Thr	Val	Ser	Asn	Leu	Ser	Met	Gln	Thr	His	Ala
			245					250				255			
Ala	Arg	Ile	Arg	Thr	Phe	Ser	Asn	Trp	Pro	Ser	Ser	Ala	Leu	Val	His
			260					265				270			
Ser	Gln	Glu	Leu	Ala	Ser	Ala	Gly	Phe	Tyr	Tyr	Thr	Gly	His	Ser	Asp
			275				280				285				
Asp	Val	Lys	Cys	Leu	Cys	Cys	Asp	Gly	Gly	Leu	Arg	Cys	Trp	Glu	Ser
			290				295				300				
Gly	Asp	Asp	Pro	Trp	Val	Glu	His	Ala	Lys	Trp	Phe	Pro	Arg	Cys	Glu
			305				310			315			320		
Tyr	Leu	Leu	Arg	Ile	Lys	Gly	Gln	Glu	Phe	Val	Ser	Gln	Val	Gln	Ala
			325					330				335			
Gly	Tyr	Pro	His	Leu	Leu	Glu	Gln	Leu	Leu	Ser	Thr	Ser	Asp	Ser	Pro
			340					345				350			
Glu	Asp	Glu	Asn	Ala	Asp	Ala	Ala	Ile	Val	His	Phe	Gly	Pro	Gly	Glu
			355					360				365			
Ser	Ser	Glu	Asp	Val	Val	Met	Met	Ser	Thr	Pro	Val	Val	Lys	Ala	Ala
			370					375				380			
Leu	Glu	Met	Gly	Phe	Ser	Arg	Ser	Leu	Val	Arg	Gln	Thr	Val	Gln	Trp
			385					390			395			400	
Gln	Ile	Leu	Ala	Thr	Gly	Glu	Asn	Tyr	Arg	Thr	Val	Ser	Asp	Leu	Val
			405						410				415		
Ile	Gly	Leu	Leu	Asp	Ala	Glu	Asp	Glu	Met	Arg	Glu	Glu	Gln	Met	Glu
			420					425				430			
Gln	Ala	Ala	Glu	Glu	Glu	Ser	Asp	Asp	Leu	Ala	Leu	Ile	Arg	Lys	
			435					440				445			
Asn	Lys	Met	Val	Leu	Phe	Gln	His	Leu	Thr	Cys	Val	Thr	Pro	Met	Leu
			450					455				460			
Tyr	Cys	Leu	Leu	Ser	Ala	Arg	Ala	Ile	Thr	Glu	Gln	Glu	Cys	Asn	Ala
			465					470			475			480	
Val	Lys	Gln	Lys	Pro	His	Thr	Leu	Gln	Ala	Ser	Thr	Leu	Ile	Asp	Thr
			485					490				495			
Val	Leu	Ala	Lys	Gly	Asn	Thr	Ala	Ala	Thr	Ser	Phe	Arg	Asn	Ser	Leu
			500					505				510			

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<210> 41  
<211> 2416  
<212> DNA  
<213> Mus musculus
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<400> 41
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caccaaaaaa cttaaacgtt taatggagaa gagccacaatc ttgtcaaatt ggacaaagga 180
gagcgaagaa aaaatgaagt ttgactttc gtgtgaactc taccgaatgt ctacatattc 240
agctttccc aggggagttc ctgttcaga gaggagtctg gtcgtgctg gcttttata 300
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gactctgctt tcagccagtc tgcaagtctcc atctaagaat atgtctcctg tgaaaagtag 480
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gagtacagaa gaggccagat ttcttactta cagttatgtgg cctttaagtt ttctgtcacc 660
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 gccaaacact gtgttag 2416

<210> 42
 <211> 591
 <212> PRT
 <213> Mus musculus

<400> 42
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 Ser Ala Phe Pro Arg Gly Val Pro Val Ser Glu Arg Ser Leu Ala Arg
 35 40 45
 Ala Gly Phe Tyr Tyr Thr Gly Val Asn Asp Lys Val Lys Cys Phe Cys
 50 55 60
 Cys Gly Leu Met Leu Asp Asn Trp Lys Gln Gly Asp Ser Pro Val Glu
 65 70 75 80
 Lys His Arg Gln Phe Tyr Pro Ser Cys Ser Phe Val Gln Thr Leu Leu
 85 90 95
 Ser Ala Ser Leu Gln Ser Pro Ser Lys Asn Met Ser Pro Val Lys Ser
 100 105 110
 Arg Phe Ala His Ser Ser Pro Leu Glu Arg Gly Gly Ile His Ser Asn
 115 120 125
 Leu Cys Ser Ser Pro Leu Asn Ser Arg Ala Val Glu Asp Phe Ser Ser
 130 135 140
 Arg Met Asp Pro Cys Ser Tyr Ala Met Ser Thr Glu Glu Ala Arg Phe
 145 150 155 160
 Leu Thr Tyr Ser Met Trp Pro Leu Ser Phe Leu Ser Pro Ala Glu Leu
 165 170 175
 Ala Arg Ala Gly Phe Tyr Tyr Ile Gly Pro Gly Asp Arg Val Ala Cys
 180 185 190
 Phe Ala Cys Gly Gly Lys Leu Ser Asn Trp Glu Pro Lys Asp Tyr Ala
 195 200 205
 Met Ser Glu His Arg Arg His Phe Pro His Cys Pro Phe Leu Glu Asn
 210 215 220
 Thr Ser Glu Thr Gln Arg Phe Ser Ile Ser Asn Leu Ser Met Gln Thr
 225 230 235 240
 His Ser Ala Arg Leu Arg Thr Phe Leu Tyr Trp Pro Pro Ser Val Pro
 245 250 255
 Val Gln Pro Glu Gln Leu Ala Ser Ala Gly Phe Tyr Tyr Val Asp Arg
 260 265 270
 Asn Asp Asp Val Lys Cys Leu Cys Cys Asp Gly Gly Leu Arg Cys Trp
 275 280 285
 Glu Pro Gly Asp Asp Pro Trp Ile Glu His Ala Lys Trp Phe Pro Arg
 290 295 300
 Cys Glu Phe Leu Ile Arg Met Lys Gly Gln Glu Phe Val Asp Glu Ile
 305 310 315 320

Gln	Ala	Arg	Tyr	Pro	His	Leu	Leu	Glu	Gln	Leu	Leu	Ser	Thr	Ser	Asp
						325				330					335
Thr	Pro	Gly	Glu	Glu	Asn	Ala	Asp	Pro	Thr	Glu	Thr	Val	Val	His	Phe
						340				345					350
Gly	Pro	Gly	Glu	Ser	Ser	Lys	Asp	Val	Val	Met	Met	Ser	Thr	Pro	Val
						355			360						365
Val	Lys	Ala	Ala	Leu	Glu	Met	Gly	Phe	Ser	Arg	Ser	Leu	Val	Arg	Gln
						370			375						380
Thr	Val	Gln	Arg	Gln	Ile	Leu	Ala	Thr	Gly	Glu	Asn	Tyr	Arg	Thr	Val
						385			390			395			400
Asn	Asp	Ile	Val	Ser	Val	Leu	Leu	Asn	Ala	Glu	Asp	Glu	Arg	Arg	Glu
						405			410						415
Glu	Glu	Lys	Glu	Arg	Gln	Thr	Glu	Glu	Met	Ala	Ser	Gly	Asp	Leu	Ser
						420			425						430
Leu	Ile	Arg	Lys	Asn	Arg	Met	Ala	Leu	Phe	Gln	Gln	Leu	Thr	His	Val
						435			440						445
Leu	Pro	Ile	Leu	Asp	Asn	Leu	Leu	Glu	Ala	Ser	Val	Ile	Thr	Lys	Gln
						450			455						460
Glu	His	Asp	Ile	Ile	Arg	Gln	Lys	Thr	Gln	Ile	Pro	Leu	Gln	Ala	Arg
						465			470			475			480
Glu	Leu	Ile	Asp	Thr	Val	Leu	Val	Lys	Gly	Asn	Ala	Ala	Asn	Ile	
						485			490						495
Phe	Lys	Asn	Ser	Leu	Lys	Gly	Ile	Asp	Ser	Thr	Leu	Tyr	Glu	Asn	Leu
						500			505						510
Phe	Val	Glu	Lys	Asn	Met	Lys	Tyr	Ile	Pro	Thr	Glu	Asp	Val	Ser	Gly
						515			520						525
Leu	Ser	Leu	Glu	Glu	Leu	Arg	Arg	Leu	Gln	Glu	Glu	Arg	Thr	Cys	
						530			535						540
Lys	Val	Cys	Met	Asp	Arg	Glu	Val	Ser	Ile	Val	Phe	Ile	Pro	Cys	Gly
						545			550			555			560
His	Leu	Val	Val	Cys	Gln	Glu	Cys	Ala	Pro	Ser	Leu	Arg	Lys	Cys	Pro
						565			570						575
Ile	Cys	Arg	Gly	Thr	Ile	Lys	Gly	Thr	Val	Arg	Thr	Phe	Leu	Ser	
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<210> 43
<211> 11
<212> PRT
<213> artificial sequence based on Homo sapiens

<400> 43
Met Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
1 5 10

<210> 44
<211> 635
<212> PRT
<213> artificial sequence based on Homo sapiens, Mus musculus, Cydia pomonella, and Drosophila melanogaster

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<221> VARIANT
<222> 1,2,3,635
<223> any amino acid or may be absent

<221> VARIANT
<222> (1) ... (635)
<223> Xaa = Any Amino Acid

<400> 44
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 Leu Xaa Thr Phe Xaa Xaa Phe Pro Xaa Xaa Xaa Pro Val Ser Xaa Xaa
 35 40 45
 Xaa Leu Ala Arg Ala Gly Phe Xaa Tyr Thr Gly Xaa Xaa Asp Xaa Val
 50 55 60
 Xaa Cys Phe Xaa Cys Xaa Xaa Xaa Asp Xaa Trp Xaa Xaa Gly Asp
 65 70 75 80
 Ser Xaa Xaa Xaa His Xaa Xaa Xaa Xaa Pro Xaa Cys Xaa Phe Ile
 85 90 95
 Xaa
 100 105 110
 Xaa Ser Xaa Xaa Xaa Xaa
 115 120 125
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Xaa Xaa Xaa Xaa
 130 135 140
 Xaa Xaa Xaa Xaa Arg Xaa Xaa Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 145 150 155 160
 Xaa Xaa Xaa Xaa Xaa Asp Xaa Ser Asp Xaa Xaa Xaa Xaa Xaa Xaa
 165 170 175
 Xaa Xaa Xaa Met Xaa Xaa Glu Glu Ala Arg Leu Xaa Thr Phe Xaa Xaa
 180 185 190
 Trp Pro Xaa Xaa Xaa Xaa Leu Xaa Pro Xaa Glu Leu Ala Xaa Ala Gly
 195 200 205
 Phe Tyr Tyr Xaa Gly Xaa Xaa Asp Xaa Val Xaa Cys Phe Xaa Cys Gly
 210 215 220
 Gly Lys Leu Xaa Asn Trp Glu Pro Xaa Asp Xaa Ala Xaa Ser Glu His
 225 230 235 240
 Xaa Arg His Phe Pro Xaa Cys Pro Phe Val Xaa Xaa Xaa Xaa Xaa Xaa
 245 250 255
 Xaa Phe Xaa Xaa
 260 265 270
 Ser Xaa Xaa Xaa Pro Xaa Asn Pro Xaa Met Ala Xaa Xaa Xaa Ala Arg
 275 280 285
 Xaa Xaa Thr Phe Xaa Xaa Trp Pro Xaa Ser Xaa Xaa Val Xaa Xaa Glu
 290 295 300
 Gln Leu Ala Xaa Ala Gly Phe Tyr Tyr Xaa Gly Xaa Gly Asp Xaa Val
 305 310 315 320
 Lys Cys Phe Xaa Cys Xaa Gly Gly Leu Xaa Xaa Trp Xaa Xaa Xaa Asp
 325 330 335
 Asp Pro Trp Xaa Gln His Ala Lys Trp Phe Pro Xaa Cys Xaa Tyr Leu
 340 345 350

Xaa Xaa Xaa Lys Gly Gln Glu Tyr	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa		
355	360	365	
Xaa Xaa Leu Xaa Glu Xaa Leu Xaa Xaa Thr	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa		
370	375	380	
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Xaa Pro	Xaa Xaa Xaa Xaa		
385	390	395	400
Xaa Xaa Asp Xaa Val Xaa Xaa Xaa Pro	Xaa Val Xaa Xaa Ala Xaa		
405	410	415	
Xaa Met Gly Phe Xaa Xaa Xaa Xaa Val Lys	Xaa Xaa Xaa Xaa Xaa Lys		
420	425	430	
Ile Xaa Xaa Xaa Gly Xaa Xaa Tyr	Xaa Xaa Xaa Xaa Xaa Leu Val Xaa		
435	440	445	
Asp Leu Xaa Xaa Ala Xaa Xaa Xaa Xaa Xaa Xaa	Glu Xaa Xaa Xaa		
450	455	460	
Xaa	Xaa Xaa Xaa Xaa Xaa		
465	470	475	480
Xaa	Xaa Xaa Xaa Xaa Xaa		
485	490	495	
Xaa	Xaa Xaa Xaa Xaa		
500	505	510	
Xaa Xaa Xaa Xaa Gln Xaa Xaa Leu Gln Xaa Xaa Xaa Xaa Xaa Xaa	Xaa Xaa Xaa		
515	520	525	
Xaa	Xaa Xaa Xaa Xaa Xaa		
530	535	540	
Xaa	Xaa Xaa Xaa Xaa Xaa		
545	550	555	560
Xaa Ser Xaa Glu Glu			
565	570	575	
Gln Leu Arg Arg Leu Xaa Glu Glu Xaa Leu Cys Lys Xaa Cys Met Asp			
580	585	590	
Xaa Glu Val Xaa Xaa Val Phe Xaa Pro Cys Gly His Leu Val Xaa Cys			
595	600	605	
Xaa Xaa Cys Ala Xaa Ser Val Xaa Lys Cys Pro Met Cys Arg Xaa Xaa			
610	615	620	
Ile Xaa Xaa Xaa Xaa Xaa Xaa Phe Leu Ser Xaa			
625	630	635	

<210> 45
<211> 204
<212> DNA
<213> Homo sapiens

<400> 45
gagtttaata gattaaaaac ttttgcta at ttccaagg tgtagtcctgt ttcagcatca 60
acactggcac gagcagggtt ctttatact ggtgaaggag ataccgtgcg gtgcattagt 120
tgtcatgcag ctgttagatag atggcaatat ggagactcag cagttggaag acacaggaaa 180
gtatccccaa attgcagatt tata 204

<210> 46
<211> 204
<212> DNA
<213> Homo sapiens

<400> 46
gaagaagcta gattaaagtc ctttcagaac tggccagact atgctcacct aaccccaaga 60
gagtttagcaa gtgctggact ctactacaca ggtattggtg accaagtgca gtgcgttgc 120
tgtggtgaa aactaaaaaa ttgggaacct tgtgatcgtg cctggtcaga acacaggcga 180
cactttctta attgcttctt tgtt 204

<210> 47
<211> 198
<212> DNA
<213> Homo sapiens

<400> 47
tatgaagcac ggatctttac ttttggaca tggatatact cagttacaa ggagcagctt 60
gcaagagctg gattttatgc ttttaggtgaa ggtgataaag taaagtgcgtt tcactgtgga 120
ggagggctaa ctgattggaa gcccagtgaa gacccttggg aacaacatgc taaatggtat 180
ccagggtgca aatatctg 198

<210> 48
<211> 138
<212> DNA
<213> Homo sapiens

<400> 48
gagcagctaa ggcgcctgca agaggagaag ctttgcacaa tctgtatgga tagaaatatt 60
gctatcggtt ttgttccttg tggacatcta gtcacttgta aacaatgtgc tgaagcagtt 120
gacaagtgtc ccatgtgc 138

<210> 49
<211> 204
<212> DNA
<213> Mus musculus

<400> 49
gagtttata gattaaaaac atttgctaac ttcccaagta gtagtcctgt ttcagcatca 60
acattggcgc gagctgggtt tctttatacc ggtgaaggag acaccgtgca atgtttcagt 120
tgtcatgcgg caatagatag atggcagtt ggagactcag ctgttgaaag acacaggaga 180
atatccccaa attgcagatt tata 204

<210> 50
<211> 204
<212> DNA
<213> Mus musculus

<400> 50
gaagaagcca gattgaagtc atttcagaac tggccggact atgctcattt aaccccccaga 60
gagtttagcta gtgctggcct ctactacaca ggggctgatg atcaagtgca atgcgttgc 120
tgtgggggaa aactaaaaaa ttgggaaccc tgtgatcgtg cctggtcaga acacaggaga 180
cactttccca attgctttt tgtt 204

<210> 51
<211> 198
<212> DNA
<213> Mus musculus

<400> 51
tatgaagcac ggatcgttac ttttggaca tggatatact cagttacaa ggaggcagctt 60
gcaagagctg gatttatgc tttaggtgaa ggcgataaag tgaagtgc ttccactgtgaa 120
ggagggctca cggttggaa gccaaatgtgaa gaccctggg accagcatgc taagtgc tac 180
ccagggtgca aataccta 198

<210> 52
<211> 138
<212> DNA
<213> Mus musculus

<400> 52
gagcagctaa ggcgcctaca agaggagaag ctttccaaaa tctgtatgga tagaaatatt 60
gctatcgaaa ttttcccttg tggacatctg gccacttgta aacagtgtgc agaagcagtt 120
gacaaatgtc ccatgtgc 138

<210> 53
<211> 204
<212> DNA
<213> Homo sapiens

<400> 53
gaactgtacc gaatgtctac gtattccact tttccgtctg gggttccctgt ctcagaaagg 60
agtcttgc tcgtctggttt ctattacact ggtgtaatg acaaggtaa atgcttctgt 120
tgtggcctga tgctggataa ctggaaaaga ggagacagtc ctactgaaaa gcataaaaaag 180
ttgtatccta gctgcagatt cgtt 204

<210> 54
<211> 201
<212> DNA
<213> Homo sapiens

<400> 54
gaaaatgcc aattacttac ttttccatgaca tggccattga cttttctgtc gccaacagat 60
ctggcacgag caggctttta ctacatagga cctggagaca gagttggcttg ctttgcctgt 120
ggtgtggaaaat tgagcaattt ggaaccgaag gataatgcta tgtcagaaca cctgagacat 180
tttcccaaattt gcccatttat a 201

<210> 55
<211> 204
<212> DNA
<213> Homo sapiens

<400> 55
catgcagccc gctttaaaac attcttaac tggccctcta gtgttcttagt taatcctgag 60
cagcttgc aa gtgcgggttt ttattatgtt ggtaacagtg atgatgtcaa atgctttgc 120
tgtgatggtg gactcagggtt ttggaaatct ggagatgatc catgggttca acatgccaag 180
tggttccaa ggtgtgagta ctgt 204

<210> 56
<211> 138
<212> DNA
<213> Homo sapiens

<400> 56
gaacaattgc ggagactacc agaagaaaaga acatgtaaag tgtgtatgga caaagaagtg 60
tccatagtgt ttattccttg tggcatcta gtagtatgca aagattgtgc tccttcctta 120
agaaaagtgtc ctatttgt 138

<210> 57
<211> 203
<212> DNA
<213> Mus musculus

<400> 57
agctgtacccg attgtccacg tattcagttt tcccagggg agttcctgtg tcagaaagga 60
gtctggctcg tgctggcttt tactacactg gtgccaatga caaggtaag tgcttctgct 120
gtggcctgtat gctagacaac tggaaacaag gggacagtcc catggagaag cacagaaagt 180
tgtaccccaag ctgcaacttt gta 203

<210> 58
<211> 201
<212> DNA
<213> Mus musculus

<400> 58
gagaaggcca gattactcac ctatgaaaca tggccattgt cttttctgtc accagcaaag 60
ctggccaaag caggcttcta ctacatagga cctggagata gagtggcctg ctttcgtgc 120
gatggaaac tgagcaactg ggaacgtaag gatgatgcta tgtcagagca ccagaggcat 180
ttccccagct gtccgttctt a 201

<210> 59
<211> 204
<212> DNA
<213> Mus musculus

<400> 59
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gaacttgcaa gtgcgggctt ttattataca ggacacagtg atgatgtcaa gtgttatgc 120
tgtatgttg ggctgagggtg ctgggaatct ggagatgacc cctgggtgga acatgccaag 180
tggtttccaa ggtgtgagta cttg 204

<210> 60
<211> 138
<212> DNA
<213> Mus musculus

<400> 60
gaacagtgc ggccctcccc ggaggacaga atgtgtaaag tgtgtatgga ccgagaggt 60
tccatcggtt tcattccctg tggccatctg gtcgtgtgca aagactgcgc tccctctctg 120
aggaagtgtc ccatctgt 138

<210> 61
<211> 204
<212> DNA
<213> Homo sapiens

卷之三

<400> 61
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agtcttgctc gtgctggttt ttattatact ggtgtgaatg acaaggtcaa atgcttctgt 120
tgtggccctga tgctggataa ctggaaacta ggagacagtc ctattcaaaa gcataaacag 180
ctatatccta gctgttagctt tatt 204

<210> 62

<211> 201

<212> DNA

<213> Homo sapiens

<400> 62

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ttggcaagag ctgggtttta ttatataggc cctggagata gggtagcctg cttgcctgt 120
ggtgggaagc tcagaactg ggaaccaaag gatgatgcta tgtcagaaca ccggaggcat 180
tttccaact gtccatTTT g 201
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<210> 63

<211> 204

<212> DNA

<213> Homo sapiens

<400> 63

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cagcttcaa gtgctggttt ttattatgtg ggtcgcaatg atgatgtcaa atgcttttgt 120  
tgtatggtg gctttaggtg ttggaatct ggagatgatc catgggtaga acatgccaag 180  
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<210> 64

<211> 138

<212> DNA

<213> Mus musculus

<400> 64

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tctgttgat ttattccttg tggtcatctg gtagtatgcc aggaatgtgc cccttctcta 120  
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<210> 65

<211> 204

<212> DNA

<213> Mus musculus

<400> 65

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tgtggcctga tgttggataa ctggaaacaa ggggacagtc ctgttgaaaa gcacagacag 180
ttctatccca gctgcagctt tgta 204

<210> 66

201

<212> DNA

<213> Mus musculus

<400> 66
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ctggccagag ctggcttcta ttacataggg cctggagaca gggtggcctg ttttcctgt 120
ggtgtggaaac tgagcaactg ggaaccaaag gattatgcta tgtcagagca ccgcagacat 180
tttccccact gtccatttct g 201

<210> 67
<211> 204
<212> DNA
<213> Mus musculus

<400> 67
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cagcttgc aa gtgctggatt ctattacgtg gatcgcaatg atgatgtcaa gtgccttgt 120
tgtgatggtg gctttagatg ttggAACCT ggagatgacc cctggataga acacgccaaa 180
tggttccaa ggtgtgagtt ctgt 204

<210> 68
<211> 114
<212> DNA
<213> Mus musculus

<400> 68
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catctagtag tctgccagga atgtgcccct tctctaagga agtgccccat ctgc 114

<210> 69
<211> 68
<212> PRT
<213> Homo sapiens

<400> 69
Glu Phe Asn Arg Leu Lys Thr Phe Ala Asn Phe Pro Ser Gly Ser Pro
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Val Ser Ala Ser Thr Leu Ala Arg Ala Gly Phe Leu Tyr Thr Gly Glu
20 25 30
Gly Asp Thr Val Arg Cys Phe Ser Cys His Ala Ala Val Asp Arg Trp
35 40 45
Gln Tyr Gly Asp Ser Ala Val Gly Arg His Arg Lys Val Ser Pro Asn
50 55 60
Cys Arg Phe Ile
65

<210> 70
<211> 68
<212> PRT
<213> Homo sapiens

<400> 70
Glu Glu Ala Arg Leu Lys Ser Phe Gln Asn Trp Pro Asp Tyr Ala His
1 5 10 15
Leu Thr Pro Arg Glu Leu Ala Ser Ala Gly Leu Tyr Tyr Thr Gly Ile
20 25 30

Gly Asp Gln Val Gln Cys Phe Cys Cys Gly Gly Lys Leu Lys Asn Trp
35 40 45
Glu Pro Cys Asp Arg Ala Trp Ser Glu His Arg Arg His Phe Pro Asn
50 55 60
Cys Phe Phe Val
65

<210> 71
<211> 66
<212> PRT
<213> Homo sapiens

<400> 71
Tyr Glu Ala Arg Ile Phe Thr Phe Gly Thr Trp Ile Tyr Ser Val Asn
1 5 10 15
Lys Glu Gln Leu Ala Arg Ala Gly Phe Tyr Ala Leu Gly Glu Gly Asp
20 25 30
Lys Val Lys Cys Phe His Cys Gly Gly Leu Thr Asp Trp Lys Pro
35 40 45
Ser Glu Asp Pro Trp Glu Gln His Ala Lys Trp Tyr Pro Gly Cys Lys
50 55 60
Tyr Leu
65

<210> 72
<211> 46
<212> PRT
<213> Homo sapiens

<400> 72
Glu Gln Leu Arg Arg Leu Gln Glu Glu Lys Leu Cys Lys Ile Cys Met
1 5 10 15
Asp Arg Asn Ile Ala Ile Val Phe Val Pro Cys Gly His Leu Val Thr
20 25 30
Cys Lys Gln Cys Ala Glu Ala Val Asp Lys Cys Pro Met Cys
35 40 45

<210> 73
<211> 68
<212> PRT
<213> Mus musculus

<400> 73
Glu Phe Asn Arg Leu Lys Thr Phe Ala Asn Phe Pro Ser Ser Pro
1 5 10 15
Val Ser Ala Ser Thr Leu Ala Arg Ala Gly Phe Leu Tyr Thr Gly Glu
20 25 30
Gly Asp Thr Val Gln Cys Phe Ser Cys His Ala Ala Ile Asp Arg Trp
35 40 45

Gln Tyr Gly Asp Ser Ala Val Gly Arg His Arg Arg Ile Ser Pro Asn
50 55 60
Cys Arg Phe Ile
65

<210> 74
<211> 68
<212> PRT
<213> Mus musculus

<400> 74
Glu Glu Ala Arg Leu Lys Ser Phe Gln Asn Trp Pro Asp Tyr Ala His
1 5 10 15
Leu Thr Pro Arg Glu Leu Ala Ser Ala Gly Leu Tyr Tyr Thr Gly Ala
20 25 30
Asp Asp Gln Val Gln Cys Phe Cys Cys Gly Gly Lys Leu Lys Asn Trp
35 40 45
Glu Pro Cys Asp Arg Ala Trp Ser Glu His Arg Arg His Phe Pro Asn
50 55 60
Cys Phe Phe Val
65

<210> 75
<211> 66
<212> PRT
<213> Mus musculus

<400> 75
Tyr Glu Ala Arg Ile Val Thr Phe Gly Thr Trp Ile Tyr Ser Val Asn
1 5 10 15
Lys Glu Gln Leu Ala Arg Ala Gly Phe Tyr Ala Leu Gly Glu Gly Asp
20 25 30
Lys Val Lys Cys Phe His Cys Gly Gly Leu Thr Asp Trp Lys Pro
35 40 45
Ser Glu Asp Pro Trp Asp Gln His Ala Lys Cys Tyr Pro Gly Cys Lys
50 55 60
Tyr Leu
65

<210> 76
<211> 46
<212> PRT
<213> Mus musculus

<400> 76
Glu Gln Leu Arg Arg Leu Gln Glu Glu Lys Leu Ser Lys Ile Cys Met
1 5 10 15
Asp Arg Asn Ile Ala Ile Val Phe Phe Pro Cys Gly His Leu Ala Thr
20 25 30
Cys Lys Gln Cys Ala Glu Ala Val Asp Lys Cys Pro Met Cys
35 40 45

<210> 77
<211> 68
<212> PRT
<213> Homo sapiens

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<400> 77
Glu Leu Tyr Arg Met Ser Thr Tyr Ser Thr Phe Pro Ala Gly Val Pro
      1           5           10          15
Val Ser Glu Arg Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val
      20          25          30
Asn Asp Lys Val Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp
      35          40          45
Lys Arg Gly Asp Ser Pro Thr Glu Lys His Lys Lys Leu Tyr Pro Ser
      50          55          60
Cys Arg Phe Val
65

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<210> 78
<211> 67
<212> PRT
<213> *Homo sapiens*

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<400> 78
Glu Asn Ala Arg Leu Leu Thr Phe Gln Thr Trp Pro Leu Thr Phe Leu
      1           5           10          15
Ser Pro Thr Asp Leu Ala Arg Ala Gly Phe Tyr Tyr Ile Gly Pro Gly
      20          25          30
Asp Arg Val Ala Cys Phe Ala Cys Gly Gly Lys Leu Ser Asn Trp Glu
      35          40          45
Pro Lys Asp Asn Ala Met Ser Glu His Leu Arg His Phe Pro Lys Cys
      50          55          60
Pro Phe Ile
65

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<210> 79
<211> 68
<212> PRT
<213> Homo sapiens

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<400> 79
His Ala Ala Arg Phe Lys Thr Phe Phe Asn Trp Pro Ser Ser Val Leu
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Val Asn Pro Glu Gln Leu Ala Ser Ala Gly Phe Tyr Tyr Val Gly Asn
   20         25          30
Ser Asp Asp Val Lys Cys Phe Cys Cys Asp Gly Gly Leu Arg Cys Trp
   35         40          45
Glu Ser Gly Asp Asp Pro Trp Val Gln His Ala Lys Trp Phe Pro Arg
   50         55          60
Cys Glu Tyr Leu
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~> <210> 80
<211> 46
<212> PRT
<213> Homo sapiens

<400> 80
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1 5 10 15
Asp Lys Glu Val Ser Ile Val Phe Ile Pro Cys Gly His Leu Val Val
20 25 30
Cys Lys Asp Cys Ala Pro Ser Leu Arg Lys Cys Pro Ile Cys
35 40 45

<210> 81
<211> 68
<212> PRT
<213> Mus musculus

<400> 81
Glu Leu Tyr Arg Leu Ser Thr Tyr Ser Ala Phe Pro Arg Gly Val Pro
1 5 10 15
Val Ser Glu Arg Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Ala
20 25 30
Asn Asp Lys Val Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp
35 40 45
Lys Gln Gly Asp Ser Pro Met Glu Lys His Arg Lys Leu Tyr Pro Ser
50 55 60
Cys Asn Phe Val
65

<210> 82
<211> 67
<212> PRT
<213> Mus musculus

<400> 82
Glu Lys Ala Arg Leu Leu Thr Tyr Glu Thr Trp Pro Leu Ser Phe Leu
1 5 10 15
Ser Pro Ala Lys Leu Ala Lys Ala Gly Phe Tyr Tyr Ile Gly Pro Gly
20 25 30
Asp Arg Val Ala Cys Phe Ala Cys Asp Gly Lys Leu Ser Asn Trp Glu
35 40 45
Arg Lys Asp Asp Ala Met Ser Glu His Gln Arg His Phe Pro Ser Cys
50 55 60
Pro Phe Leu
65

<210> 83
<211> 68
<212> PRT
<213> Mus musculus

<400> 83
His Ala Ala Arg Ile Arg Thr Phe Ser Asn Trp Pro Ser Ser Ala Leu
1 5 10 15
Val His Ser Gln Glu Leu Ala Ser Ala Gly Phe Tyr Tyr Thr Gly His
20 25 30
Ser Asp Asp Val Lys Cys Leu Cys Cys Asp Gly Gly Leu Arg Cys Trp
35 40 45
Glu Ser Gly Asp Asp Pro Trp Val Glu His Ala Lys Trp Phe Pro Arg
50 55 60
Cys Glu Tyr Leu
65

<210> 84
<211> 46
<212> PRT
<213> Mus musculus

<400> 84
Glu Gln Leu Arg Pro Leu Pro Glu Asp Arg Met Cys Lys Val Cys Met
1 5 10 15
Asp Arg Glu Val Ser Ile Val Phe Ile Pro Cys Gly His Leu Val Val
20 25 30
Cys Lys Asp Cys Ala Pro Ser Leu Arg Lys Cys Pro Ile Cys
35 40 45

<210> 85
<211> 68
<212> PRT
<213> Homo sapiens

<400> 85
Glu Leu Tyr Arg Met Ser Thr Tyr Ser Thr Phe Pro Ala Gly Val Pro
1 5 10 15
Val Ser Glu Arg Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val
20 25 30
Asn Asp Lys Val Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp
35 40 45
Lys Leu Gly Asp Ser Pro Ile Gln Lys His Lys Gln Leu Tyr Pro Ser
50 55 60
Cys Ser Phe Ile
65

<210> 86
<211> 67
<212> PRT
<213> Homo sapiens

<400> 86

Glu	Glu	Ala	Arg	Phe	Leu	Thr	Tyr	His	Met	Trp	Pro	Leu	Thr	Phe	Leu
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Ser	Pro	Ser	Glu	Leu	Ala	Arg	Ala	Gly	Phe	Tyr	Tyr	Ile	Gly	Pro	Gly
			20					25					30		
Asp	Arg	Val	Ala	Cys	Phe	Ala	Cys	Gly	Gly	Lys	Leu	Ser	Asn	Trp	Glu
				35				40					45		
Pro	Lys	Asp	Asp	Ala	Met	Ser	Glu	His	Arg	Arg	His	Phe	Pro	Asn	Cys
	50					55					60				
Pro	Phe	Leu													
	65														

<210> 87

<211> 68

<212> PRT

<213> Homo sapiens

<400> 87

His	Ala	Ala	Arg	Met	Arg	Thr	Phe	Met	Tyr	Trp	Pro	Ser	Ser	Val	Pro
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Val	Gln	Pro	Glu	Gln	Leu	Ala	Ser	Ala	Gly	Phe	Tyr	Tyr	Val	Gly	Arg
							20		25				30		
Asn	Asp	Asp	Val	Lys	Cys	Phe	Gly	Cys	Asp	Gly	Gly	Leu	Arg	Cys	Trp
				35			40				45				
Glu	Ser	Gly	Asp	Asp	Pro	Trp	Val	Glu	His	Ala	Lys	Trp	Phe	Pro	Arg
	50				55			60							
Cys	Glu	Phe	Leu												
	65														

<210> 88

<211> 46

<212> PRT

<213> Homo sapiens

<400> 88

Glu	Gln	Leu	Arg	Arg	Leu	Gln	Glu	Glu	Arg	Thr	Cys	Lys	Val	Cys	Met
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Asp	Lys	Glu	Val	Ser	Val	Val	Phe	Ile	Pro	Cys	Gly	His	Leu	Val	Val
							20		25			30			
Cys	Gln	Glu	Cys	Ala	Pro	Ser	Leu	Arg	Lys	Cys	Pro	Ile	Cys		
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<210> 89

<211> 68

<212> PRT

<213> Mus musculus

<400> 89
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Val Ser Glu Arg Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val
20 25 30

Asn Asp Lys Val Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp
35 40 45
Lys Gln Gly Asp Ser Pro Val Glu Lys His Arg Gln Phe Tyr Pro Ser
50 55 60
Cys Ser Phe Val
65

<210> 90
<211> 67
<212> PRT
<213> Mus musculus

<400> 90
Glu Glu Ala Arg Phe Leu Thr Tyr Ser Met Trp Pro Leu Ser Phe Leu
1 5 10 15
Ser Pro Ala Glu Leu Ala Arg Ala Gly Phe Tyr Tyr Ile Gly Pro Gly
20 25 30
Asp Arg Val Ala Cys Phe Ala Cys Gly Gly Lys Leu Ser Asn Trp Glu
35 40 45
Pro Lys Asp Tyr Ala Met Ser Glu His Arg Arg His Phe Pro His Cys
50 55 60
Pro Phe Leu
65

<210> 91
<211> 68
<212> PRT
<213> Mus musculus

<400> 91
His Ser Ala Arg Leu Arg Thr Phe Leu Tyr Trp Pro Pro Ser Val Pro
1 5 10 15
Val Gln Pro Glu Gln Leu Ala Ser Ala Gly Phe Tyr Tyr Val Asp Arg
20 25 30
Asn Asp Asp Val Lys Cys Leu Cys Cys Asp Gly Gly Leu Arg Cys Trp
35 40 45
Glu Pro Gly Asp Asp Pro Trp Ile Glu His Ala Lys Trp Phe Pro Arg
50 55 60
Cys Glu Phe Leu
65

<210> 92
<211> 38
<212> PRT
<213> Mus musculus

<400> 92
Glu Arg Thr Cys Lys Val Cys Met Asp Arg Glu Val Ser Ile Val Phe
1 5 10 15
Ile Pro Cys Gly His Leu Val Val Cys Gln Glu Cys Ala Pro Ser Leu
20 25 30
Arg Lys Cys Pro Ile Cys
35

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Korneluk, Robert G.
Mackenzie, Alexander E.
Baird, Stephen

(ii) TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
PROBES, AND DETECTION METHODS

(iii) NUMBER OF SEQUENCES: 42

(iv) CORRESPONDENCE ADDRESS:

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- (C) CITY: Boston
- (D) STATE: MA
- (E) COUNTRY: USA
- (F) ZIP: 02110-2804

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/511,485
- (B) FILING DATE: 04-AUG-1995
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Clark, Paul T.
- (B) REGISTRATION NUMBER: 30,162
- (C) REFERENCE/DOCKET NUMBER: 07891/002001

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 617/542-5070
- (B) TELEFAX: 617/542-8906
- (C) TELEX: 200154

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa at positons 2, 3, 4, 5,

6, 7, 9, 10, 11, 17, 18, 19, 20, 21, 23, 25, 30, 31, 32, 34, 35, 38, 39, 40, 41, 42, and 45 may be any amino acid. Xaa at position 8 is Glu or Asp. Xaa at positions 14 & 22 is Val or Ile.

(xi) SEQUENCE DESCRIPTION: SEQ_ID_NO:1:

Glu	Xaa	Cys	Lys	Xaa	Cys	Met							
1									10				15
Xaa Xaa Xaa Xaa Xaa Xaa Phe Xaa Pro Cys Gly His Xaa Xaa Xaa													
									25				30
Cys Xaa Xaa Cys Ala Xaa Xaa Xaa Xaa Cys Pro Xaa Cys													
									40				45

(2) INFORMATION FOR SEQ_ID_NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa at positions 1, 2, 3, 6, 9, 10, 14, 15, 18, 19, 20, 21, 24, 30, 32, 33, 35, 37, 40, 42, 43, 44, 45, 46, 47, 49, 50, 51, 53, 54, 55, 56, 57, 59, 60, 61, 62, 64 and 66 may be any amino acid. Xaa at positions 13, 16 and 17 may be any amino acid or may be absent.

(xi) SEQUENCE DESCRIPTION: SEQ_ID_NO:2:

Xaa	Xaa	Xaa	Arg	Leu	Xaa	Thr	Phe	Xaa	Xaa	Trp	Pro	Xaa	Xaa	Xaa
1				5						10				15
Xaa Xaa Xaa Xaa Leu Ala Xaa Ala Gly Phe Tyr Tyr Xaa Gly Xaa														
										25				30
Xaa Asp Xaa Val Xaa Cys Phe Xaa Cys Xaa Xaa Xaa Xaa Xaa Trp														
										35				45
Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Xaa His Xaa Xaa Xaa Xaa Pro Xaa														
										50				60
Cys Xaa Phe Val														
										65				

(2) INFORMATION FOR SEQ_ID_NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAAAAGGTGG ACAAGTCCTA TTTTCAAGAG AAGATGACTT TTAACAGTTT TGAAGGATCT	60
AAAACTTGTG TACCTGCAGA CATCAATAAG GAAGAAGAAT TTGTTAGAAGA GTTTAATAGA	120
TTAAAAACTT TTGCTAATT TCCAAGTGGT AGTCCTGTT CAGCATCAC ACTGGCACGA	180
GCAGGGTTTC TTTATACGG TGAAGGAGAT ACCGTGCGGT GCTTTAGTTG TCATGCAGCT	240
GTAGATAGAT GGCAATATGG AGACTCAGCA GTTGGAAAGAC ACAGGAAAGT ATCCCCAAAT	300
TGCAGATT TA CAACGGCTT TTATCTTGAA AATAGTGCCTA CGCAGTCTAC AAATTCTGGT	360
ATCCAGAATG GTCAGTACAA AGTTGAAAAC TATCTGGAA GCAGAGATCA TTTTGCCTTA	420
GACAGGCCAT CTGAGACACA TGCAGACTAT CTTTGAGAA CTGGGCAGGT TGTAGATATA	480
TCAGACACCA TATACCCGAG GAACCCTGCC ATGTATTGTG AAGAAGCTAG ATTAAAGTCC	540
TTTCAGAACT GGCCAGACTA TGCTCACCTA ACCCCAAGAG AGTTAGCAAG TGCTGGACTC	600
TACTACACAG GTATTGGTGA CCAAGTGCAG TGCTTTGTT GTGGTGGAAA ACTGAAAAAT	660
TGGGAACCTT GTGATCGTGC CTGGTCAGAA CACAGGCGAC ACTTTCTAA TTGCTTCTTT	720
GTTTGGGCC GGAATCTAA TATTCGAAGT GAATCTGATG CTGTGAGTTC TGATAGGAAT	780
TTCCCAAATT CAACAAATCT TCCAAGAAAT CCATCCATGG CAGATTATGA AGCACGGATC	840
TTTACTTTG GGACATGGAT ATACTCAGTT ACAAAGGAGC AGCTTGCAAG AGCTGGATTT	900
TATGCTTTAG GTGAAGGTGA TAAAGTAAAG TGCTTCACT GTGGAGGAGG GCTAACTGAT	960
TGGAAGCCC GTGAAGACCC TTGGGAACAA CATGCTAAAT GGTATCCAGG GTGCAAATAT	1020
CTGTTAGAAC AGAAGGGACA AGAATATATA ACAAATATTC ATTTAACTCA TTCACTTGAG	1080
GAGTGTCTGG TAAGAACTAC TGAGAAAACA CCATCACTAA CTAGAAGAAT TGATGATACC	1140
ATCTTCCAAA ATCCTATGGT ACAAGAAGCT ATACGAATGG GGTCAGTTT CAAGGACATT	1200
AAGAAAATAA TGGAGGAAAA AATTCAAGATA TCTGGGAGCA ACTATAAATC ACTTGAGGTT	1260
CTGGTTGCAG ATCTAGTGA TGCTCAGAAA GACAGTATGC AAGATGAGTC AAGTCAGACT	1320
TCATTACAGA AAGAGATTAG TACTGAAGAG CAGCTAAGGC GCCTGCAAGA GGAGAAGCTT	1380
TGCAAATCT GTATGGATAG AAATATTGCT ATCGTTTTG TTCTTGTGG ACATCTAGTC	1440
ACTTGAAAC AATGTGCTGA AGCAGTTGAC AAGTGTCCC TGTGCTACAC AGTCATTACT	1500
TTCAAGCAAA AAATTTTAT GTCTTAATCT AACTCTATAG TAGGCATGTT ATGTTGTTCT	1560
TATTACCCCTG ATTGAATGTG TGATGTGAAC TGACTTTAAG TAATCAGGAT TGAATTCCAT	1620
TAGCATTGTC TACCAAGTAG GAAAAAAAAT GTACATGGCA GTGTTTAGT TGGCAATATA	1680
ATCTTGAAT TTCTTGATTT TTCAGGGTAT TAGCTGTATT ATCCATTCTT TTTACTGTTA	1740

TTTAATTGAA ACCATAGACT AAGAATAAGA AGCATCATAAC TATAACTGAA CACAATGTGT 1800
 ATTCATAGTA TACTGATTAA ATTCTAAAGT GTAAGTGAAT TAATCATCTG GATTTTTAT 1860
 TCTTTCAAGA TAGGCTTAAC AAATGGAGCT TTCTGTATAT AAATGTGGAG ATTAGAGTTA 1920
 ATCTCCCCAA TCACATAATT TGTTTGTGT GAAAAAGGAA TAAATTGTTCCATGCTGGTG 1980
 GAAAGATAGA GATTGTTTT AGAGGTTGGT TGTTGTGTT TAGGATTCTG TCCATTTCT 2040
 TGAAAGGGAA TAAACACGGA CGTGTGCGAA ATATGTTGT AAAGTGAATT GCCATTGTTG 2100
 AAAGCGTATT TAATGATAGA ATACTATCGA GCCAACATGT ACTGACATGG AAAGATGTCA 2160
 GAGATATGTT AAGTGTAAA TGCAAGTGGC GGGACACTAT GTATAGTCTG AGCCAGATCA 2220
 AAGTATGTAT GTTGTAAATA TGCATAGAAC GAGAGATTG GAAAGATATA CACCAAACGT 2280
 TTAAATGTGG TTTCTCTTCG GGGAGGGGGG GATTGGGGGA GGGGCCAG AGGGGTTTTA 2340
 GAGGGGCCTT TTCACTTTCG ACTTTTTCA TTTTGTCTG TTCGGATT TTATAAGTAT 2400
 GTAGACCCCG AAGGGTTTA TGGGAACCTAA CATCAGTAAC CTAACCCCCG TGACTATCCT 2460
 GTGCTCTTCC TAGGGAGCTG TGTTGTTCC CACCCACCAC CCTTCCCTCT GAACAAATGC 2520
 CTGAGTGCTG GGGCACTTTN 2540

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 497 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Thr	Phe	Asn	Ser	Phe	Glu	Gly	Ser	Lys	Thr	Cys	Val	Pro	Ala	Asp
1									10					15	
Ile	Asn	Lys	Glu	Glu	Glu	Phe	Val	Glu	Glu	Phe	Asn	Arg	Leu	Lys	Thr
									25				30		
Phe	Ala	Asn	Phe	Pro	Ser	Gly	Ser	Pro	Val	Ser	Ala	Ser	Thr	Leu	Ala
									40			45			
Arg	Ala	Gly	Phe	Leu	Tyr	Thr	Gly	Glu	Gly	Asp	Thr	Val	Arg	Cys	Phe
									55			60			
Ser	Cys	His	Ala	Ala	Val	Asp	Arg	Trp	Gln	Tyr	Gly	Asp	Ser	Ala	Val
									70			75		80	
Gly	Arg	His	Arg	Lys	Val	Ser	Pro	Asn	Cys	Arg	Phe	Ile	Asn	Gly	Phe
									85			90		95	
Tyr	Leu	Glu	Asn	Ser	Ala	Thr	Gln	Ser	Thr	Asn	Ser	Gly	Ile	Gln	Asn

100

105

110

Gly Gln Tyr Lys Val Glu Asn Tyr Leu Gly Ser Arg Asp His Phe Ala
 115 120 125

Leu Asp Arg Pro Ser Glu Thr His Ala Asp Tyr Leu Leu Arg Thr Gly
 130 135 140

Gln Val Val Asp Ile Ser Asp Thr Ile Tyr Pro Arg Asn Pro Ala Met
 145 150 155 160

Tyr Cys Glu Glu Ala Arg Leu Lys Ser Phe Gln Asn Trp Pro Asp Tyr
 165 170 175

Ala His Leu Thr Pro Arg Glu Leu Ala Ser Ala Gly Leu Tyr Tyr Thr
 180 185 190

Gly Ile Gly Asp Gln Val Gln Cys Phe Cys Cys Gly Gly Lys Leu Lys
 195 200 205

Asn Trp Glu Pro Cys Asp Arg Ala Trp Ser Glu His Arg Arg His Phe
 210 215 220

Pro Asn Cys Phe Phe Val Leu Gly Arg Asn Leu Asn Ile Arg Ser Glu
 225 230 235 240

Ser Asp Ala Val Ser Ser Asp Arg Asn Phe Pro Asn Ser Thr Asn Leu
 245 250 255

Pro Arg Asn Pro Ser Met Ala Asp Tyr Glu Ala Arg Ile Phe Thr Phe
 260 265 270

Gly Thr Trp Ile Tyr Ser Val Asn Lys Glu Gln Leu Ala Arg Ala Gly
 275 280 285

Phe Tyr Ala Leu Gly Glu Gly Asp Lys Val Lys Cys Phe His Cys Gly
 290 295 300

Gly Gly Leu Thr Asp Trp Lys Pro Ser Glu Asp Pro Trp Glu Gln His
 305 310 315 320

Ala Lys Trp Tyr Pro Gly Cys Lys Tyr Leu Leu Glu Gln Lys Gly Gln
 325 330 335

Glu Tyr Ile Asn Asn Ile His Leu Thr His Ser Leu Glu Glu Cys Leu
 340 345 350

Val Arg Thr Thr Glu Lys Thr Pro Ser Leu Thr Arg Arg Ile Asp Asp
 355 360 365

Thr Ile Phe Gln Asn Pro Met Val Gln Glu Ala Ile Arg Met Gly Phe
 370 375 380

Ser Phe Lys Asp Ile Lys Lys Ile Met Glu Glu Lys Ile Gln Ile Ser
 385 390 395 400

Gly Ser Asn Tyr Lys Ser Leu Glu Val Leu Val Ala Asp Leu Val Asn
 405 410 415

Ala Gln Lys Asp Ser Met Gln Asp Glu Ser Ser Gln Thr Ser Leu Gln
 420 425 430

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Lys Glu Ile Ser Thr Glu Glu Gln Leu Arg Arg Leu Gln Glu Glu Lys
435 440 445

Leu Cys Lys Ile Cys Met Asp Arg Asn Ile Ala Ile Val Phe Val Pro
450 455 460

Cys Gly His Leu Val Thr Cys Lys Gln Cys Ala Glu Ala Val Asp Lys
465 470 475 480

Cys Pro Met Cys Tyr Thr Val Ile Thr Phe Lys Gln Lys Ile Phe Met
485 490 495

Ser

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2676 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCCTTGAGAT GTATCA GTATCA GTATCA AGGATTAGG ATCTCCATGT TGGAACTCTA AATGCATAGA	60
AATGGAAATA ATGGAAATTT TTCATTTGG CTTTCAGCC TAGTATTAAA ACTGATAAAA	120
GCAAAGCCAT GCACAAAACT ACCTCCCTAG AGAAAGGCTA GTCCCTTTTC TTCCCCATTC	180
ATTCATTAT GAACATAGTA GAAAACAGCA TATTCTTATC AAATTTGATG AAAAGCGCCA	240
ACACGTTGA ACTGAAATAC GACTTGTCA GTGAACGTGA CCGAATGTCT ACGTATTCCA	300
CTTTTCCTGC TGGGGTTCCT GTCTCAGAAA GGAGTCTTGC TCGTGCTGGT TTCTATTACA	360
CTGGTGTGAA TGACAAGGTC AAATGCTTCT GTTGTGGCCT GATGCTGGAT AACTGGAAAA	420
GAGGAGACAG TCCTACTGAA AAGCATAAAA AGTTGTATCC TAGCTGCAGA TTCGTTCAGA	480
GTCTAAATTC CGTTAACAAAC TTGGAAAGCTA CCTCTCAGCC TACTTTCTC TCTTCAGTAA	540
CACATTCCAC ACACTCATTA CTTCCGGGTA CAGAAAACAG TGGATATTTC CGTGGCTCTT	600
ATTCAAACTC TCCATCAAAT CCTGTAAACT CCAGAGCAAA TCAAGAATTT TCTGCCTTGA	660
TGAGAAAGTTC CTACCCCTGT CCAATGAATA ACGAAAATGC CAGATTACTT ACTTTTCAGA	720
CATGGCCATT GACTTTCTG TCGCCAACAG ATCTGGCACG AGCAGGCTTT TACTACATAG	780
GACCTGGAGA CAGAGTGGCT TGCTTGCCT GTGGTGGAAA ATTGAGGAAT TGGGAACCGA	840
AGGATAATGC TATGTCAGAA CACCTGAGAC ATTTCCCAA ATGCCCATTT ATAGAAAATC	900
AGCTTCAAGA CACTTCAAGA TACACAGTTT CTAATCTGAG CATGCAGACA CATGCAGCCC	960

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GCTTTAAAAC ATTCTTAAC TGGCCCTCTA GTGTTCTAGT TAATCCTGAG CAGCTTGCAA	1020
GTGCGGGTTT TTATTATGTG GGTAACAGTG ATGATGTCAA ATGCTTTGC TGTGATGGTG	1080
GAECTCAGGTG TTGGGAATCT GGAGATGATC CATGGTTCA ACATGCCAAG TGTTTCCAA	1140
GGTGTGAGTA CTTGATAAGA ATTAAGGAC AGGAGTTCAT CCGTCAGTT CAAGCCAGTT	1200
ACCCTCATCT ACTTGAACAG CTGCTATCCA CATCAGACAG CCCAGGAGAT GAAAATGCAG	1260
AGTCATCAAT TATCCATTG GAACCTGGAG AAGACCATTG AGAAGATGCA ATCATGATGA	1320
ATACTCCTGT GATTAATGCT GCCGTGGAAA TGGGCTTAG TAGAACCTG GTAAAACAGA	1380
CAGTTCAGAG AAAAATCCTA GCAACTGGAG AGAATTATAG ACTAGTCAT GATCTGTGT	1440
TAGACTTACT CAATGCAGAA GATGAAATAA GGGAGAGGA GAGAGAAAGA GCAACTGAGG	1500
AAAAAGAACATC AAATGATTAA TTATTAAATCC GGAAGAATAG AATGGCACTT TTTCAACATT	1560
TGACTTGTGT AATTCCAATC CTGGATAGTC TACTAACTGC CGAACATTATT AATGAACAAG	1620
AACATGATGT TATTAAACAG AAGACACAGA CGTCTTTACA AGCAAGAGAA CTGATTGATA	1680
CGATTTAGT AAAAGGAAAT ATTGCAGCCA CTGTATTGAG AAACTCTCTG CAAGAAGCTG	1740
AAGCTGTGTT ATATGAGCAT TTATTTGTGC AACAGGACAT AAAATATATT CCCACAGAAG	1800
ATGTTTCAGA TCTACCAGTG GAAGAACAAAT TGCGGAGACT ACCAGAAGAA AGAACATGTA	1860
AAGTGTGTAT GGACAAAGAA GTGTCCATAG TGTTTATTCC TTGTGGTCAT CTAGTAGTAT	1920
GCAAAGATTG TGCTCCTTCT TTAAGAAAGT GTCCTATTG TAGGAGTACA ATCAAGGGTA	1980
CAGTCGTAC ATTTCTTCA TGAAGAAGAA CCAAAACATC GTCTAAACTT TAGAATTAAT	2040
TTATTAAATG TATTATAACT TTAACCTTTA TCCTAATTG GTTCTCTAA AATTTTATT	2100
TATTTACAAC TCAAAAAACA TTGTTTGTG TAACATATTT ATATATGTAT CTAAACCATA	2160
TGAACATATA TTTTTAGAA ACTAAGAGAA TGATAGGCTT TTGTTCTTAT GAACGAAAAA	2220
GAGGTAGCAC TACAAACACA ATATTCAATC CAAATTCAG CATTATTGAA ATTGTAAGTG	2280
AAGTAAAAC TAAAGATATT GAGTTAACCT TTAAGAATT TAAATATTG GGCATTGTAC	2340
TAATACCGGG AACATGAAGC CAGGTGTGGT GGTATGTACC TGTAGTCCC GGCTGAGGCA	2400
AGAGAATTAC TTGAGCCAG GAGTTGAAT CCATCCTGGG CAGCATACTG AGACCCCTGCC	2460
TTTAAAAACN AACAGNACCA AANCCAAACA CCAGGGACAC ATTTCTCTGT CTTTTTGAT	2520
CAGTGTCTA TACATCGAAG GTGTGCATAT ATGTTGAATC ACATTTAGG GACATGGTGT	2580
TTTTATAAAG AATTCTGTGA GNAAAATTT AATAAAGCAA CCAAATTACT CTTAAAAAAA	2640
AAAAAAAAAAA AAAAAACTCG AGGGGCCCGT ACCAAT	2676

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 604 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Asn Ile Val Glu Asn Ser Ile Phe Leu Ser Asn Leu Met Lys Ser
1 5 10 15

Ala Asn Thr Phe Glu Leu Lys Tyr Asp Leu Ser Cys Glu Leu Tyr Arg
20 25 30

Met Ser Thr Tyr Ser Thr Phe Pro Ala Gly Val Pro Val Ser Glu Arg
35 40 45

Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val Asn Asp Lys Val
50 55 60

Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp Lys Arg Gly Asp
65 70 75 80

Ser Pro Thr Glu Lys His Lys Lys Leu Tyr Pro Ser Cys Arg Phe Val
85 90 95

Gln Ser Leu Asn Ser Val Asn Asn Leu Glu Ala Thr Ser Gln Pro Thr
100 105 110

Phe Pro Ser Ser Val Thr His Ser Thr His Ser Leu Leu Pro Gly Thr
115 120 125

Glu Asn Ser Gly Tyr Phe Arg Gly Ser Tyr Ser Asn Ser Pro Ser Asn
130 135 140

Pro Val Asn Ser Arg Ala Asn Gln Glu Phe Ser Ala Leu Met Arg Ser
145 150 155 160

Ser Tyr Pro Cys Pro Met Asn Asn Glu Asn Ala Arg Leu Leu Thr Phe
165 170 175

Gln Thr Trp Pro Leu Thr Phe Leu Ser Pro Thr Asp Leu Ala Arg Ala
180 185 190

Gly Phe Tyr Tyr Ile Gly Pro Gly Asp Arg Val Ala Cys Phe Ala Cys
195 200 205

Gly Gly Lys Leu Ser Asn Trp Glu Pro Lys Asp Asn Ala Met Ser Glu
210 215 220

His Leu Arg His Phe Pro Lys Cys Pro Phe Ile Glu Asn Gln Leu Gln
225 230 235 240

Asp Thr Ser Arg Tyr Thr Val Ser Asn Leu Ser Met Gln Thr His Ala
245 250 255

Ala Arg Phe Lys Thr Phe Phe Asn Trp Pro Ser Ser Val Leu Val Asn
260 265 270

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Pro Glu Gln Leu Ala Ser Ala Gly Phe Tyr Tyr Val Gly Asn Ser Asp
275 280 285

Asp Val Lys Cys Phe Cys Cys Asp Gly Gly Leu Arg Cys Trp Glu Ser
290 295 300

Gly Asp Asp Pro Trp Val Gln His Ala Lys Trp Phe Pro Arg Cys Glu
305 310 315 320

Tyr Leu Ile Arg Ile Lys Gly Gln Glu Phe Ile Arg Gln Val Gln Ala
325 330 335

Ser Tyr Pro His Leu Leu Glu Gln Leu Leu Ser Thr Ser Asp Ser Pro
340 345 350

Gly Asp Glu Asn Ala Glu Ser Ser Ile Ile His Leu Glu Pro Gly Glu
355 360 365

Asp His Ser Glu Asp Ala Ile Met Met Asn Thr Pro Val Ile Asn Ala
370 375 380

Ala Val Glu Met Gly Phe Ser Arg Ser Leu Val Lys Gln Thr Val Gln
385 390 395 400

Arg Lys Ile Leu Ala Thr Gly Glu Asn Tyr Arg Leu Val Asn Asp Leu
405 410 415

Val Leu Asp Leu Leu Asn Ala Glu Asp Glu Ile Arg Glu Glu Glu Arg
420 425 430

Glu Arg Ala Thr Glu Glu Lys Glu Ser Asn Asp Leu Leu Ile Arg
435 440 445

Lys Asn Arg Met Ala Leu Phe Gln His Leu Thr Cys Val Ile Pro Ile
450 455 460

Leu Asp Ser Leu Leu Thr Ala Gly Ile Ile Asn Glu Gln Glu His Asp
465 470 475 480

Val Ile Lys Gln Lys Thr Gln Thr Ser Leu Gln Ala Arg Glu Leu Ile
485 490 495

Asp Thr Ile Leu Val Lys Gly Asn Ile Ala Ala Thr Val Phe Arg Asn
500 505 510

Ser Leu Gln Glu Ala Glu Ala Val Leu Tyr Glu His Leu Phe Val Gln
515 520 525

Gln Asp Ile Lys Tyr Ile Pro Thr Glu Asp Val Ser Asp Leu Pro Val
530 535 540

Glu Glu Gln Leu Arg Arg Leu Pro Glu Glu Arg Thr Cys Lys Val Cys
545 550 555 560

Met Asp Lys Glu Val Ser Ile Val Phe Ile Pro Cys Gly His Leu Val
565 570 575

Val Cys Lys Asp Cys Ala Pro Ser Leu Arg Lys Cys Pro Ile Cys Arg
580 585 590

Ser Thr Ile Lys Gly Thr Val Arg Thr Phe Leu Ser
595 600

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2580 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTAGGTTACC TGAAAGAGTT ACTACAACCC CAAAGAGTTG TGTCTAAGT AGTATCTTGG	60
TAATTCAAGAG AGATAACTCAT CCTACCTGAA TATAAACTGA GATAAAATCCA GTAAAGAAAG	120
TGTAGTAAAT TCTACATAAG AGTCTATCAT TGATTCTTT TTGTGGTGGAA AATCTTAGTT	180
CATGTGAAGA AATTCATGT GAATGTTTA GCTATCAAAC AGTACTGTCA CCTACTCATG	240
CACAAAACGT CCTCCCAAAG ACTTTCCCA GGTCCCTCGT ATCAAAACAT TAAGAGTATA	300
ATGGAAGATA GCACGATCTT GTCAGATTGG ACAAAACAGCA ACAAAACAAAA AATGAAGTAT	360
GACTTTCCCT GTGAACTCTA CAGAATGTCT ACATATTCAA CTTTCCCCGC CGGGGTGCCT	420
GTCTCAGAAA GGAGTCTTGC TCGTGCTGGT TTTTATTATA CTGGTGTGAA TGACAAGGTC	480
AAATGCTTCT GTTGTGGCCT GATGCTGGAT AACTGGAAAC TAGGAGACAG TCCTATTCAA	540
AAGCATAAAC AGCTATATCC TAGCTGTAGC TTTATTCAA ATCTGGTTTC AGCTAGTCTG	600
GGATCCACCT CTAAGAATAC GTCTCCAATG AGAAACAGTT TTGCACATTC ATTATCTCCC	660
ACCTTGGAAC ATAGTAGCTT GTTCAGTGGT TCTTACTCCA GCCTTCCCT AAACCCCTCTT	720
AATTCTAGAG CAGTTGAAGA CATCTCTTCA TCGAGGACTA ACCCCTACAG TTATGCAATG	780
AGTACTGAAG AAGCCAGATT TCTTACCTAC CATATGTGGC CATTAACTTT TTTGTACCCA	840
TCAGAATTGG CAAGAGCTGG TTTTATTAT ATAGGACCTG GAGATAGGGT AGCCTGCTTT	900
GCCTGTGGTG GGAAGCTCAG TAACTGGAA CCAAAGGATG ATGCTATGTC AGAACACCGG	960
AGGCATTTTC CCAACTGTCC ATTTTGAA AATTCTCTAG AAACTCTGAG GTTACGATT	1020
TCAAATCTGA GCATGCAGAC ACATGCAGCT CGAATGAGAA CATTATGTA CTGGCCATCT	1080
AGTGTCCAG TTCAGCCTGA GCAGCTTGCAG AGTGTGGTT TTTATTATGT GGGTCGCAAT	1140
GATGATGTCA AATGCTTGG TTGTGATGGT GGCTTGAGGT GTGGGAATC TGGAGATGAT	1200
CCATGGGTAG AACATGCCAA GTGGTTCCA AGGTGTGAGT TCTTGATACG AATGAAAGGC	1260
CAAGAGTTG TTGATGAGAT TCAAGGTAGA TATCCTCATC TTCTGAACA GCTGTGTCA	1320
ACTTCAGATA CCACTGGAGA AGAAAATGCT GACCCACCAA TTATTCATTT TGGACCTGGAA	1380
GAAAGTTCTT CAGAAGATGC TGTCATGATG AATACACCTG TGGTTAAATC TGCCTTGGAA	1440

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ATGGGCTTA ATAGAGACCT GGTGAAACAA ACAGTTCTAA GTAAAATCCT GACAAC TGGA	1500
GAGAACTATA AAACAGTTAA TGATATTGTG TCAGCACTTC TTAATGCTGA AGATGAAAAA	1560
AGAGAAGAGG AGAAGGAAAA ACAAGCTGAA GAAATGGCAT CAGATGATTG GTCATTAATT	1620
CGGAAGAACAA GAATGGCTCT CTTTCAACAA TTGACATGTG TGCTTCCTAT CCTGGATAAT	1680
CTTTAAAGG CCAATGTAAT TAATAAACAG GAACATGATA TTATTAACAA AAAAACACAG	1740
ATACCTTAC AAGCGAGAGA ACTGATTGAT ACCATTGGG TTAAAGGAAA TGCTGCCGCC	1800
AACATCTTCA AAAACTGTCT AAAAGAAATT GACTCTACAT TGTATAAGAA CTTATTTGTG	1860
GATAAGAATA TGAAGTATAT TCCAACAGAA GATGTTTCAG GTCTGTCACT GGAAGAACAA	1920
TTGAGGAGGT TGCAAGAAGA ACGAACTTGT AAAGTGTGTA TGGACAAAGA AGTTTCTGTT	1980
GTATTTATTCTT CTTGTTGTC TCTGGTAGTA TGCCAGGAAT GTGCCCTTC TCTAAGAAAA	2040
TGCCCTATTGCAGGGGTAT AATCAAGGGT ACTGTTCGTA CATTCTCTC TTAAAGAAAA	2100
ATAGTCTATA TTTAACCTG CATAAAAGG TCTTAAAT ATTGTTAAC ACTTGAAGCC	2160
ATCTAAAGTA AAAAGGAAT TATGAGTTT TCAATTAGTA ACATTCTGT TCTAGTCTGC	2220
TTTGGTACTA ATAATCTTGT TTCTGAAAG ATGGTATCAT ATATTAATC TTAATCTGTT	2280
TATTTACAAG GGAAGATTAA TGTTGGTGA ACTATATTAG TATGTATGTG TACCTAAGGG	2340
AGTAGCGTCN CTGCTTGTAA TGCACTCATTT CAGGAGTTAC TGGATTGTT GTTCTTCAG	2400
AAAGCTTGA ANACTAAATT ATAGTGTAGA AAAGAACTGG AAACCAGGAA CTCTGGAGTT	2460
CATCAGAGTT ATGGTGCCGA ATTGTCTTG GTGCTTTCA CTTGTGTTT AAAATAAGGA	2520
TTTTCTCTT ATTTCTCCCC CTAGTTGTG AGAAACATCT CAATAAGTG CTTAAAAAG	2580

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 618 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met His Lys Thr Ala Ser Gln Arg Leu Phe Pro Gly Pro Ser Tyr Gln	
1 5 10 15	
Asn Ile Lys Ser Ile Met Glu Asp Ser Thr Ile Leu Ser Asp Trp Thr	
20 25 30	
Asn Ser Asn Lys Gln Lys Met Lys Tyr Asp Phe Ser Cys Glu Leu Tyr	
35 40 45	

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Arg	Met	Ser	Thr	Tyr	Ser	Thr	Phe	Pro	Ala	Gly	Val	Pro	Val	Ser	Glu
50							55				60				
Arg	Ser	Leu	Ala	Arg	Ala	Gly	Phe	Tyr	Tyr	Thr	Gly	Val	Asn	Asp	Lys
65				70					75			80			
Val	Lys	Cys	Phe	Cys	Cys	Gly	Leu	Met	Leu	Asp	Asn	Trp	Lys	Leu	Gly
							85		90				95		
Asp	Ser	Pro	Ile	Gln	Lys	His	Lys	Gln	Leu	Tyr	Pro	Ser	Cys	Ser	Phe
								100		105			110		
Ile	Gln	Asn	Leu	Val	Ser	Ala	Ser	Leu	Gly	Ser	Thr	Ser	Lys	Asn	Thr
								115		120			125		
Ser	Pro	Met	Arg	Asn	Ser	Phe	Ala	His	Ser	Leu	Ser	Pro	Thr	Leu	Glu
							130		135			140			
His	Ser	Ser	Leu	Phe	Ser	Gly	Ser	Tyr	Ser	Ser	Leu	Pro	Pro	Asn	Pro
							145		150			155			160
Leu	Asn	Ser	Arg	Ala	Val	Glu	Asp	Ile	Ser	Ser	Ser	Arg	Thr	Asn	Pro
							165			170			175		
Tyr	Ser	Tyr	Ala	Met	Ser	Thr	Glu	Glu	Ala	Arg	Phe	Leu	Thr	Tyr	His
							180			185			190		
Met	Trp	Pro	Leu	Thr	Phe	Leu	Ser	Pro	Ser	Glu	Leu	Ala	Arg	Ala	Gly
							195			200			205		
Phe	Tyr	Tyr	Ile	Gly	Pro	Gly	Asp	Arg	Val	Ala	Cys	Phe	Ala	Cys	Gly
							210			215			220		
Gly	Lys	Leu	Ser	Asn	Trp	Glu	Pro	Lys	Asp	Asp	Ala	Met	Ser	Glu	His
							225			230			235		240
Arg	Arg	His	Phe	Pro	Asn	Cys	Pro	Phe	Leu	Glu	Asn	Ser	Leu	Glu	Thr
							245			250			255		
Leu	Arg	Phe	Ser	Ile	Ser	Asn	Leu	Ser	Met	Gln	Thr	His	Ala	Ala	Arg
							260			265			270		
Met	Arg	Thr	Phe	Met	Tyr	Trp	Pro	Ser	Ser	Val	Pro	Val	Gln	Pro	Glu
							275			280			285		
Gln	Leu	Ala	Ser	Ala	Gly	Phe	Tyr	Tyr	Val	Gly	Arg	Asn	Asp	Asp	Val
							290			295			300		
Lys	Cys	Phe	Gly	Cys	Asp	Gly	Gly	Leu	Arg	Cys	Trp	Glu	Ser	Gly	Asp
							305			310			315		320
Asp	Pro	Trp	Val	Glu	His	Ala	Lys	Trp	Phe	Pro	Arg	Cys	Glu	Phe	Leu
							325			330			335		
Ile	Arg	Met	Lys	Gly	Gln	Glu	Phe	Val	Asp	Glu	Ile	Gln	Gly	Arg	Tyr
							340			345			350		
Pro	His	Leu	Leu	Glu	Gln	Leu	Leu	Ser	Thr	Ser	Asp	Thr	Thr	Gly	Glu
							355			360			365		
Glu	Asn	Ala	Asp	Pro	Pro	Ile	Ile	His	Phe	Gly	Pro	Gly	Glu	Ser	Ser
							370			375			380		

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Ser Glu Asp Ala Val Met Met Asn Thr Pro Val Val Lys Ser Ala Leu
385 390 395 400

Glu Met Gly Phe Asn Arg Asp Leu Val Lys Gln Thr Val Leu Ser Lys
405 410 415

Ile Leu Thr Thr Gly Glu Asn Tyr Lys Thr Val Asn Asp Ile Val Ser
420 425 430

Ala Leu Leu Asn Ala Glu Asp Glu Lys Arg Glu Glu Lys Glu Lys
435 440 445

Gln Ala Glu Glu Met Ala Ser Asp Asp Leu Ser Leu Ile Arg Lys Asn
450 455 460

Arg Met Ala Leu Phe Gln Gln Leu Thr Cys Val Leu Pro Ile Leu Asp
465 470 475 480

Asn Leu Leu Lys Ala Asn Val Ile Asn Lys Gln Glu His Asp Ile Ile
485 490 495

Lys Gln Lys Thr Gln Ile Pro Leu Gln Ala Arg Glu Leu Ile Asp Thr
500 505 510

Ile Trp Val Lys Gly Asn Ala Ala Asn Ile Phe Lys Asn Cys Leu
515 520 525

Lys Glu Ile Asp Ser Thr Leu Tyr Lys Asn Leu Phe Val Asp Lys Asn
530 535 540

Met Lys Tyr Ile Pro Thr Glu Asp Val Ser Gly Leu Ser Leu Glu Glu
545 550 555 560

Gln Leu Arg Arg Leu Gln Glu Glu Arg Thr Cys Lys Val Cys Met Asp
565 570 575

Lys Glu Val Ser Val Val Phe Ile Pro Cys Gly His Leu Val Val Cys
580 585 590

Gln Glu Cys Ala Pro Ser Leu Arg Lys Cys Pro Ile Cys Arg Gly Ile
595 600 605

Ile Lys Gly Thr Val Arg Thr Phe Leu Ser
610 615

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2100 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GACACTCTGC TGGGCGGCCGG GCCGCCCTCC TCCGGGACCT CCCCTCGGGA ACCGTCGCC 60

GCGGCGCTTA	GTTAGGACTG	GAGTGCTTGG	CGCGAAAAGG	TGGACAAGTC	CTATTTCCA	120
GAGAAGATGA	CTTTAACAG	TTTGAAAGGA	ACTAGAACTT	TTGTACTTGC	AGACACCAAT	180
AAGGATGAAG	AATTGTAGA	AGAGTTAAT	AGATTAAGAA	CATTTGCTAA	CTTCCCAAGT	240
AGTAGTCCTG	TTTCAGCATH	AACATTGGCG	CGAGCTGGGT	TTCTTATAC	CGGTGAAGGA	300
GACACCGTGC	AATGTTTCAG	TTGTCATGCG	GCAATAGATA	GATGGCAGTA	TGGAGACTCA	360
GCTGTTGGAA	GACACAGGAG	AATATCCCCA	AATTGCAGAT	TTATCAATGG	TTTTTATTTT	420
GAAAATGGTG	CTGCACAGTC	TACAAATCCT	GGTATCCAAA	ATGCCAGTA	CAAATCTGAA	480
AACTGTGTGG	GAAATAGAAA	TCCTTTGCC	CCTGACAGGC	CACCTGAGAC	TCATGCTGAT	540
TATCTCTTGA	GAACCTGGACA	GGTTGTAGAT	ATTCAGACA	CCATATAACCC	GAGGAACCCCT	600
GCCATGTGTA	GTGAAGAACG	CAGATTGAAG	TCATTCAGA	ACTGGCCGGA	CTATGCTCAT	660
TTAACCCCCA	GAGAGTTAGC	TAGTGCTGGC	CTCTACTACA	CAGGGGCTGA	TGATCAAGTG	720
CAATGCTTTT	GTTGTGGGGG	AAAAACTGAAA	AATTGGGAAAC	CCTGTGATCG	TGCCTGGTCA	780
GAACACAGGA	GACACTTCC	CAATTGCTTT	TTTGTGTTGG	GCCGGAACGT	TAATGTTCGA	840
AGTGAATCTG	GTGTGAGTTC	TGATAGGAAT	TTCCCAAATT	CAACAAACTC	TCCAAGAAAT	900
CCAGCCATGG	CAGAATATGA	AGCACGGATC	GTTACTTTG	GAACATGGAT	ATACTCAGTT	960
AACAAGGAGC	AGCTTGCAAG	AGCTGGATT	TATGCTTTAG	GTGAAGGCAG	TAAAGTGAAG	1020
TGCTTCCACT	GTGGAGGAGG	GTCACGGAT	TGGAAGCCAA	GTGAAGACCC	CTGGGACCAG	1080
CATGCTAAGT	GCTACCCAGG	GTGCAAATAC	CTATTGGATG	AGAAGGGCA	AGAATATATA	1140
AATAATATTC	ATTTAACCCA	TCCACTTGAG	GAATCTTGG	GAAGAACTGC	TGAAAAAAACA	1200
CCACCGCTAA	CTAAAAAAAT	CGATGATACC	ATCTTCCAGA	ATCCTATGGT	GCAAGAAGCT	1260
ATACGAATGG	GATTTAGCTT	CAAGGACCTT	AAGAAAACAA	TGGAAGAAAA	AATCCAAACA	1320
TCCGGGAGCA	GCTATCTATC	ACTTGAGGTC	CTGATTGCAG	ATCTTGTGAG	TGCTCAGAAA	1380
GATAATACGG	AGGATGAGTC	AAAGTCAAACT	TCATTGCAGA	AAGACATTAG	TACTGAAGAG	1440
CAGCTAAGGC	GCCTACAAGA	GGAGAAAGCTT	TCCAAAATCT	GTATGGATAG	AAATATTGCT	1500
ATCGTTTTT	TTCTCTGTGG	ACATCTGGCC	ACTTGTAAAC	AGTGTGCAGA	AGCAGTTGAC	1560
AAATGTCCC	TGTGCTACAC	CGTCATTACG	TTCAACCAAA	AAATTTTAT	GTCTTAGTGG	1620
GGCACCCACAT	GTTATGTTCT	TCTTGCTCTA	ATTGAATGTG	TAATGGGAGC	GAACTTAACG	1680
TAATCCTGCA	TTTGCAATTCC	ATTAGCATCC	TGCTGTTCC	AAATGGGAGAC	CAATGCTAAC	1740
AGCACTGTT	CCGCTAAAC	ATTCAATTTC	TGGATCTTTC	GAGTTATCAG	CTGTATCATT	1800
TAGCCAGTGT	TTTACTCGAT	TGAAACCTTA	GACAGAGAAG	CATTTTATAG	CTTTTCACAT	1860
GTATATTGGT	AGTACACTGA	CTTGATTTCT	ATATGTAAGT	GAATTCACTCA	CCTGCATGTT	1920

TCATGCCTT TGCATAAGCT TAACAAATGG AGTGTCTGT ATAAGCATGG AGATGTGATG	1980
GAATCTGCC AATGACTTTA ATTGGCTTAT TGTAACACG GAAAGAACTG CCCCACGCTG	2040
CTGGGAGGAT AAAGATTGTT TTAGATGCTC ACTTCTGTGT TTTAGGATTC TGCCCATTAA	2100

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 496 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Thr Phe Asn Ser Phe Glu Gly Thr Arg Thr Phe Val Leu Ala Asp			
1	5	10	15
Thr Asn Lys Asp Glu Glu Phe Val Glu Glu Phe Asn Arg Leu Lys Thr			
20	25	30	
Phe Ala Asn Phe Pro Ser Ser Pro Val Ser Ala Ser Thr Leu Ala			
35	40	45	
Arg Ala Gly Phe Leu Tyr Thr Gly Glu Gly Asp Thr Val Gln Cys Phe			
50	55	60	
Ser Cys His Ala Ala Ile Asp Arg Trp Gln Tyr Gly Asp Ser Ala Val			
65	70	75	80
Gly Arg His Arg Arg Ile Ser Pro Asn Cys Arg Phe Ile Asn Gly Phe			
85	90	95	
Tyr Phe Glu Asn Gly Ala Ala Gln Ser Thr Asn Pro Gly Ile Gln Asn			
100	105	110	
Gly Gln Tyr Lys Ser Glu Asn Cys Val Gly Asn Arg Asn Pro Phe Ala			
115	120	125	
Pro Asp Arg Pro Pro Glu Thr His Ala Asp Tyr Leu Leu Arg Thr Gly			
130	135	140	
Gln Val Val Asp Ile Ser Asp Thr Ile Tyr Pro Arg Asn Pro Ala Met			
145	150	155	160
Cys Ser Glu Glu Ala Arg Leu Lys Ser Phe Gln Asn Trp Pro Asp Tyr			
165	170	175	
Ala His Leu Thr Pro Arg Glu Leu Ala Ser Ala Gly Leu Tyr Tyr Thr			
180	185	190	
Gly Ala Asp Asp Gln Val Gln Cys Phe Cys Cys Gly Gly Lys Leu Lys			
195	200	205	
Asn Trp Glu Pro Cys Asp Arg Ala Trp Ser Glu His Arg Arg His Phe			

210

215

220

Pro Asn Cys Phe Phe Val Leu Gly Arg Asn Val Asn Val Arg Ser Glu		
225	230	235
<hr/>		
Ser Gly Val Ser Ser Asp Arg Asn Phe Pro Asn Ser Thr Asn Ser Pro		
245	250	255
<hr/>		
Arg Asn Pro Ala Met Ala Glu Tyr Glu Ala Arg Ile Val Thr Phe Gly		
260	265	270
<hr/>		
Thr Trp Ile Tyr Ser Val Asn Lys Glu Gln Leu Ala Arg Ala Gly Phe		
275	280	285
<hr/>		
Tyr Ala Leu Gly Glu Gly Asp Lys Val Lys Cys Phe His Cys Gly Gly		
290	295	300
<hr/>		
Gly Leu Thr Asp Trp Lys Pro Ser Glu Asp Pro Trp Asp Gln His Ala		
305	310	315
<hr/>		
Lys Cys Tyr Pro Gly Cys Lys Tyr Leu Leu Asp Glu Lys Gly Gln Glu		
325	330	335
<hr/>		
Tyr Ile Asn Asn Ile His Leu Thr His Pro Leu Glu Glu Ser Leu Gly		
340	345	350
<hr/>		
Arg Thr Ala Glu Lys Thr Pro Pro Leu Thr Lys Lys Ile Asp Asp Thr		
355	360	365
<hr/>		
Ile Phe Gln Asn Pro Met Val Gln Glu Ala Ile Arg Met Gly Phe Ser		
370	375	380
<hr/>		
Phe Lys Asp Leu Lys Lys Thr Met Glu Glu Lys Ile Gln Thr Ser Gly		
385	390	395
<hr/>		
Ser Ser Tyr Leu Ser Leu Glu Val Leu Ile Ala Asp Leu Val Ser Ala		
405	410	415
<hr/>		
Gln Lys Asp Asn Thr Glu Asp Glu Ser Ser Gln Thr Ser Leu Gln Lys		
420	425	430
<hr/>		
Asp Ile Ser Thr Glu Glu Gln Leu Arg Arg Leu Gln Glu Glu Lys Leu		
435	440	445
<hr/>		
Ser Lys Ile Cys Met Asp Arg Asn Ile Ala Ile Val Phe Phe Pro Cys		
450	455	460
<hr/>		
Gly His Leu Ala Thr Cys Lys Gln Cys Ala Glu Ala Val Asp Lys Cys		
465	470	475
<hr/>		
Pro Met Cys Tyr Thr Val Ile Thr Phe Asn Gln Lys Ile Phe Met Ser		
485	490	495

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 67 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Lys Ala Ala Arg Leu Gly Thr Tyr Thr Asn Trp Pro Val Gln Phe Leu
1 5 10 15
Glu Pro Ser Arg Met Ala Ala Ser Gly Phe Tyr Tyr Leu Gly Arg Gly
20 25 30
Asp Glu Val Arg Cys Ala Phe Cys Lys Val Glu Ile Thr Asn Trp Val
35 40 45
Arg Gly Asp Asp Pro Glu Thr Asp His Lys Arg Trp Ala Pro Gln Cys
50 55 60
Pro Phe Val
65

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 275 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Ser Asp Leu Arg Leu Glu Glu Val Arg Leu Asn Thr Phe Glu Lys
1 5 10 15
Trp Pro Val Ser Phe Leu Ser Pro Glu Thr Met Ala Lys Asn Gly Phe
20 25 30
Tyr Tyr Leu Gly Arg Ser Asp Glu Val Arg Cys Ala Phe Cys Lys Val
35 40 45
Glu Ile Met Arg Trp Lys Glu Gly Glu Asp Pro Ala Ala Asp His Lys
50 55 60
Lys Trp Ala Pro Gln Cys Pro Phe Val Lys Gly Ile Asp Val Cys Gly
65 70 75 80
Ser Ile Val Thr Thr Asn Asn Ile Gln Asn Thr Thr His Asp Thr
85 90 95
Ile Ile Gly Pro Ala His Pro Lys Tyr Ala His Glu Ala Ala Arg Val
100 105 110
Lys Ser Phe His Asn Trp Pro Arg Cys Met Lys Gln Arg Pro Glu Gln
115 120 125
Met Ala Asp Ala Gly Phe Phe Tyr Thr Gly Tyr Gly Asp Asn Thr Lys

130 135 140

Cys Phe Tyr Cys Asp Gly Gly Leu Lys Asp Trp Glu Pro Glu Asp Val
 145 150 155 160

Pro Trp Glu Gln His Val Arg Trp Phe Asp Arg Cys Ala Tyr Val Gln
 165 170 175

Leu Val Lys Gly Arg Asp Tyr Val Gln Lys Val Ile Thr Glu Ala Cys
 180 185 190

Val Leu Pro Gly Glu Asn Thr Thr Val Ser Thr Ala Ala Pro Val Ser
 195 200 205

Glu Pro Ile Pro Glu Thr Lys Ile Glu Lys Glu Pro Gln Val Glu Asp
 210 215 220

Ser Lys Leu Cys Lys Ile Cys Tyr Val Glu Glu Cys Ile Val Cys Phe
 225 230 240

Val Pro Cys Gly His Val Val Ala Cys Ala Lys Cys Ala Leu Ser Val
 245 250 255

Asp Lys Cys Pro Met Cys Arg Lys Ile Val Thr Ser Val Leu Lys Val
 260 265 270

Tyr Phe Ser
 275

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 498 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Thr Glu Leu Gly Met Glu Leu Glu Ser Val Arg Leu Ala Thr Phe
 1 5 10 15

Gly Glu Trp Pro Leu Asn Ala Pro Val Ser Ala Glu Asp Leu Val Ala
 20 25 30

Asn Gly Phe Phe Ala Thr Gly Lys Trp Leu Glu Ala Glu Cys His Phe
 35 40 45

Cys His Val Arg Ile Asp Arg Trp Glu Tyr Gly Asp Gln Val Ala Glu
 50 55 60

Arg His Arg Arg Ser Ser Pro Ile Cys Ser Met Val Leu Ala Pro Asn
 65 70 75 80

His Cys Gly Asn Val Pro Arg Ser Gln Glu Ser Asp Asn Glu Gly Asn
 85 90 95

Ser Val Val Asp Ser Pro Glu Ser Cys Ser Cys Pro Asp Leu Leu Leu
 100 105 110
 Glu Ala Asn Arg Leu Val Thr Phe Lys Asp Trp Pro Asn Pro Asn Ile
 115 120 125
 Thr Pro Gln Ala Leu Ala Lys Ala Gly Phe Tyr Tyr Leu Asn Arg Leu
 130 135 140
 Asp His Val Lys Cys Val Trp Cys Asn Gly Val Ile Ala Lys Trp Glu
 145 150 155 160
 Lys Asn Asp Asn Ala Phe Glu Glu His Lys Arg Phe Phe Pro Gln Cys
 165 170 175
 Pro Arg Val Gln Met Gly Pro Leu Ile Glu Phe Ala Thr Gly Lys Asn
 180 185 190
 Leu Asp Glu Leu Gly Ile Gln Pro Thr Thr Leu Pro Leu Arg Pro Lys
 195 200 205
 Tyr Ala Cys Val Asp Ala Arg Leu Arg Thr Phe Thr Asp Trp Pro Ile
 210 215 220
 Ser Asn Ile Gln Pro Ala Ser Ala Leu Ala Gln Ala Gly Leu Tyr Tyr
 225 230 235 240
 Gln Lys Ile Gly Asp Gln Val Arg Cys Phe His Cys Asn Ile Gly Leu
 245 250 255
 Arg Ser Trp Gln Lys Glu Asp Glu Pro Trp Phe Glu His Ala Lys Trp
 260 265 270
 Ser Pro Lys Cys Gln Phe Val Leu Leu Ala Lys Gly Pro Ala Tyr Val
 275 280 285
 Ser Glu Val Leu Ala Thr Thr Ala Ala Asn Ala Ser Ser Gln Pro Ala
 290 295 300
 Thr Ala Pro Ala Pro Thr Leu Gln Ala Asp Val Leu Met Asp Glu Ala
 305 310 315 320
 Pro Ala Lys Glu Ala Leu Thr Leu Gly Ile Asp Gly Gly Val Val Arg
 325 330 335
 Asn Ala Ile Gln Arg Lys Leu Leu Ser Ser Gly Cys Ala Phe Ser Thr
 340 345 350
 Leu Asp Glu Leu Leu His Asp Ile Phe Asp Asp Ala Gly Ala Gly Ala
 355 360 365
 Ala Leu Glu Val Arg Glu Pro Pro Glu Pro Ser Ala Pro Phe Ile Glu
 370 375 380
 Pro Cys Gln Ala Thr Thr Ser Lys Ala Ala Ser Val Pro Ile Pro Val
 385 390 395 400
 Ala Asp Ser Ile Pro Ala Lys Pro Gln Ala Ala Glu Ala Val Ser Asn
 405 410 415
 Ile Ser Lys Ile Thr Asp Glu Ile Gln Lys Met Ser Val Ser Thr Pro
 420 425 430

Asn Gly Asn Leu Ser Leu Glu Glu Asn Arg Gln Leu Lys Asp Ala
435 440 445

Arg Leu Cys Lys Val Cys Leu Asp Glu Glu Val Gly Val Val Phe Leu
450 455 460

Pro Cys Gly His Leu Ala Thr Cys Asn Gln Cys Ala Pro Ser Val Ala
465 470 475 480

Asn Cys Pro Met Cys Arg Ala Asp Ile Lys Gly Phe Val Arg Thr Phe
485 490 495

Leu Ser

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Glu Glu Val Arg Leu Asn Thr Phe Glu Lys Trp Pro Val Ser Phe Leu
1 5 10 15

Ser Pro Glu Thr Met Ala Lys Asn Gly Phe Tyr Tyr Leu Gly Arg Ser
20 25 30

Asp Glu Val Arg Cys Ala Phe Cys Lys Val Glu Ile Met Arg Trp Lys
35 40 45

Glu Gly Glu Asp Pro Ala Ala Asp His Lys Lys Trp Ala Pro Gln Cys
50 55 60

Pro Phe Val
65

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Glu Ala Asn Arg Leu Val Thr Phe Lys Asp Trp Pro Asn Pro Asn Ile
1 5 10 15

Thr Pro Gln Ala Leu Ala Lys Ala Gly Phe Tyr Tyr Leu Asn Arg Leu
20 25 30

Asp His Val Lys Cys Val Trp Cys Asn Gly Val Ile Ala Lys Trp Glu
35 40 45

Lys Asn Asp Asn Ala Phe Glu Glu His Lys Arg Phe Phe Pro Gln Cys
50 55 60

Pro Arg Val
65

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Glu Phe Asn Arg Leu Lys Thr Phe Ala Asn Phe Pro Ser Ser Ser Pro
1 5 10 15

Val Ser Ala Ser Thr Leu Ala Arg Ala Gly Phe Leu Tyr Thr Gly Glu
20 25 30

Gly Asp Thr Val Gln Cys Phe Ser Cys His Ala Ala Ile Asp Arg Trp
35 40 45

Gln Tyr Gly Asp Ser Ala Val Gly Arg His Arg Arg Ile Ser Pro Asn
50 55 60

Cys Arg Phe Ile
65

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Glu Phe Asn Arg Leu Lys Thr Phe Ala Asn Phe Pro Ser Gly Ser Pro
1 5 10 15

Val Ser Ala Ser Thr Leu Ala Arg Ala Gly Phe Leu Tyr Thr Gly Glu
20 25 30

Gly Asp Thr Val Arg Cys Phe Ser Cys His Ala Ala Val Asp Arg Trp
35 40 45

Gln Tyr Gly Asp Ser Ala Val Gly Arg His Arg Lys Val Ser Pro Asn
50 55 60

Cys Arg Phe Ile
65

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Glu Leu Tyr Arg Met Ser Thr Tyr Ser Thr Phe Pro Ala Gly Val Pro
1 5 10 15

Val Ser Glu Arg Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val
20 25 30

Asn Asp Lys Val Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp
35 40 45

Lys Arg Gly Asp Ser Pro Thr Glu Lys His Lys Lys Leu Tyr Pro Ser
50 55 60

Cys Arg Phe Val
65

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Glu Leu Tyr Arg Met Ser Thr Tyr Ser Thr Phe Pro Ala Gly Val Pro
1 5 10 15

Val Ser Glu Arg Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val
20 25 30

Asn Asp Lys Val Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp
35 40 45

Lys Leu Gly Asp Ser Pro Ile Gln Lys His Lys Gln Leu Tyr Pro Ser
50 55 60
Cys Ser Phe Ile
65

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: both
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Glu Glu Ala Arg Leu Lys Ser Phe Gln Asn Trp Pro Asp Tyr Ala His
1 5 10 15
Leu Thr Pro Arg Glu Leu Ala Ser Ala Gly Leu Tyr Tyr Thr Gly Ala
20 25 30
Asp Asp Gln Val Gln Cys Phe Cys Cys Gly Gly Lys Leu Lys Asn Trp
35 40 45
Glu Pro Cys Asp Arg Ala Trp Ser Glu His Arg Arg His Phe Pro Asn
50 55 60
Cys Phe Phe Val
65

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Glu Glu Ala Arg Leu Lys Ser Phe Gln Asn Trp Pro Asp Tyr Ala His
1 5 10 15
Leu Thr Pro Arg Glu Leu Ala Ser Ala Gly Leu Tyr Tyr Thr Gly Ile
20 25 30
Gly Asp Gln Val Gln Cys Phe Cys Cys Gly Gly Lys Leu Lys Asn Trp
35 40 45
Glu Pro Cys Asp Arg Ala Trp Ser Glu His Arg Arg His Phe Pro Asn
50 55 60

Cys Phe Phe Val
65

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Glu Asn Ala Arg Leu Leu Thr Phe Gln Thr Trp Pro Leu Thr Phe Leu
1 5 10 15

Ser Pro Thr Asp Leu Ala Arg Ala Gly Phe Tyr Tyr Ile Gly Pro Gly
20 25 30

Asp Arg Val Ala Cys Phe Ala Cys Gly Gly Lys Leu Ser Asn Trp Glu
35 40 45

Pro Lys Asp Asn Ala Met Ser Glu His Leu Arg His Phe Pro Lys Cys
50 55 60

Pro Phe Ile
65

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Glu Glu Ala Arg Phe Leu Thr Tyr His Met Trp Pro Leu Thr Phe Leu
1 5 10 15

Ser Pro Ser Glu Leu Ala Arg Ala Gly Phe Tyr Tyr Ile Gly Pro Gly
20 25 30

Asp Arg Val Ala Cys Phe Ala Cys Gly Gly Lys Leu Ser Asn Trp Glu
35 40 45

Pro Lys Asp Asp Ala Met Ser Glu His Arg Arg His Phe Pro Asn Cys
50 55 60

Pro Phe Leu
65

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Tyr Glu Ala Arg Ile Val Thr Phe Gly Thr Trp Ile Tyr Ser Val Asn
1 5 10 15

Lys Glu Gln Leu Ala Arg Ala Gly Phe Tyr Ala Leu Gly Glu Gly Asp
20 25 30

Lys Val Lys Cys Phe His Cys Gly Gly Leu Thr Asp Trp Lys Pro
35 40 45

Ser Glu Asp Pro Trp Asp Gln His Ala Lys Cys Tyr Pro Gly Cys Lys
50 55 60

Tyr Leu
65

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Tyr Glu Ala Arg Ile Phe Thr Phe Gly Thr Trp Ile Tyr Ser Val Asn
1 5 10 15

Lys Glu Gln Leu Ala Arg Ala Gly Phe Tyr Ala Leu Gly Glu Gly Asp
20 25 30

Lys Val Lys Cys Phe His Cys Gly Gly Leu Thr Asp Trp Lys Pro
35 40 45

Ser Glu Asp Pro Trp Glu Gln His Ala Lys Trp Tyr Pro Gly Cys Lys
50 55 60

Tyr Leu.
65

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 68 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

His	Ala	Ala	Arg	Phe	Lys	Thr	Phe	Phe	Asn	Trp	Pro	Ser	Ser	Val	Leu
1				5					10						15
Val	Asn	Pro	Glu	Gln	Leu	Ala	Ser	Ala	Gly	Phe	Tyr	Tyr	Val	Gly	Asn
	20						25							30	
Ser	Asp	Asp	Val	Lys	Cys	Phe	Cys	Cys	Asp	Gly	Gly	Leu	Arg	Cys	Trp
	35					40						45			
Glu	Ser	Gly	Asp	Asp	Pro	Trp	Val	Gln	His	Ala	Lys	Trp	Phe	Pro	Arg
	50				55						60				
Cys	Glu	Tyr	Leu												
	65														

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 68 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

His	Ala	Ala	Arg	Met	Arg	Thr	Phe	Met	Tyr	Trp	Pro	Ser	Ser	Val	Pro
1				5				10							15
Val	Gln	Pro	Glu	Gln	Leu	Ala	Ser	Ala	Gly	Phe	Tyr	Tyr	Val	Gly	Arg
	20						25						30		
Asn	Asp	Asp	Val	Lys	Cys	Phe	Gly	Cys	Asp	Gly	Gly	Leu	Arg	Cys	Trp
	35					40						45			
Glu	Ser	Gly	Asp	Asp	Pro	Trp	Val	Glu	His	Ala	Lys	Trp	Phe	Pro	Arg
	50				55						60				
Cys	Glu	Phe	Leu												
	65														

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 68 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Glu Ala Ala Arg Leu Arg Thr Phe Ala Glu Trp Pro Arg Gly Leu Lys
1 5 10 15

Gln Arg Pro Glu Glu Leu Ala Glu Ala Gly Phe Phe Tyr Thr Gly Gln
20 25 30

Gly Asp Lys Thr Arg Cys Phe Cys Cys Asp Gly Gly Leu Lys Asp Trp
35 40 45

Glu Pro Asp Asp Ala Pro Trp Gln Gln His Ala Arg Trp Tyr Asp Arg
50 55 60

Cys Glu Tyr Val
65

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Glu Ala Ala Arg Val Lys Ser Phe His Asn Trp Pro Arg Cys Met Lys
1 5 10 15

Gln Arg Pro Glu Gln Met Ala Asp Ala Gly Phe Phe Tyr Thr Gly Tyr
20 25 30

Gly Asp Asn Thr Lys Cys Phe Tyr Cys Asp Gly Gly Leu Lys Asp Trp
35 40 45

Glu Pro Glu Asp Val Pro Trp Glu Gln His Val Arg Trp Phe Asp Arg
50 55 60

Cys Ala Tyr Val
65

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Val Asp Ala Arg Leu Arg Thr Phe Thr Asp Trp Pro Ile Ser Asn Ile
1 5 10 15

Gln Pro Ala Ser Ala Leu Ala Gln Ala Gly Leu Tyr Tyr Gln Lys Ile
20 25 30

Gly Asp Gln Val Arg Cys Phe His Cys Asn Ile Gly Leu Arg Ser Trp
35 40 45

Gln Lys Glu Asp Glu Pro Trp Phe Glu His Ala Lys Trp Ser Pro Lys
50 55 60

Cys Gln Phe Val
65

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(iii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Glu Ser Val Arg Leu Ala Thr Phe Gly Glu Trp Pro Leu Asn Ala Pro
1 5 10 15

Val Ser Ala Glu Asp Leu Val Ala Asn Gly Phe Phe Gly Thr Trp Met
20 25 30

Glu Ala Glu Cys Asp Phe Cys His Val Arg Ile Asp Arg Trp Glu Tyr
35 40 45

Gly Asp Leu Val Ala Glu Arg His Arg Arg Ser Ser Pro Ile Cys Ser
50 55 60

Met Val
65

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: r

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Glu	Gln	Leu	Arg	Arg	Leu	Gln	Glu	Glu	Arg	Thr	Cys	Lys	Val	Cys	Met
1					5				10					15	
Asp	Lys	Glu	Val	Ser	Val	Val	Phe	Ile	Pro	Cys	Gly	His	Leu	Val	Val
					20			25					30		
Cys	Gln	Glu	Cys	Ala	Pro	Ser	Leu	Arg	Lys	Cys	Pro	Ile	Cys		
					35			40				45			

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 46 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Glu	Gln	Leu	Arg	Arg	Leu	Pro	Glu	Glu	Arg	Thr	Cys	Lys	Val	Cys	Met
1					5				10				15		
Asp	Lys	Glu	Val	Ser	Ile	Val	Phe	Ile	Pro	Cys	Gly	His	Leu	Val	Val
					20			25					30		
Cys	Lys	Asp	Cys	Ala	Pro	Ser	Leu	Arg	Lys	Cys	Pro	Ile	Cys		
					35			40				45			

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 46 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Glu	Gln	Leu	Arg	Arg	Leu	Gln	Glu	Glu	Lys	Leu	Ser	Lys	Ile	Cys	Met
1					5				10				15		
Asp	Arg	Asn	Ile	Ala	Ile	Val	Phe	Phe	Pro	Cys	Gly	His	Leu	Ala	Thr
					20			25					30		
Cys	Lys	Gln	Cys	Ala	Glu	Ala	Val	Asp	Lys	Cys	Pro	Met	Cys		

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 amino acids
(B) TYPE:-amino-acid-
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Glu	Gln	Leu	Arg	Arg	Leu	Gln	Glu	Glu	Lys	Leu	Cys	Lys	Ile	Cys	Met
1					5				10				15		
Asp	Arg	Asn	Ile	Ala	Ile	Val	Phe	Val	Pro	Cys	Gly	His	Leu	Val	Thr
			20					25				30			
Cys	Lys	Gln	Cys	Ala	Glu	Ala	Val	Asp	Lys	Cys	Pro	Met	Cys		
			35					40				45			

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Glu	Glu	Asn	Arg	Gln	Leu	Lys	Asp	Ala	Arg	Leu	Cys	Lys	Val	Cys	Leu
1					5				10				15		
Asp	Glu	Glu	Val	Gly	Val	Val	Phe	Leu	Pro	Cys	Gly	His	Leu	Ala	Thr
			20					25				30			
Cys	Asn	Gln	Cys	Ala	Pro	Ser	Val	Ala	Asn	Cys	Pro	Met	Cys		
			35					40				45			

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Glu	Lys	Glu	Pro	Gln	Val	Glu	Asp	Ser	Lys	Leu	Cys	Lys	Ile	Cys	Tyr
1				5					10				15		
Val	Glu	Glu	Cys	Ile	Val	Cys	Phe	Val	Pro	Cys	Gly	His	Val	Val	Ala
	20					25						30			
Cys	Ala	Lys	Cys	Ala	Leu	Ser	Val	Asp	Lys	Cys	Pro	Met	Cys		
	35					40						45			

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Ala	Val	Glu	Ala	Glu	Val	Ala	Asp	Asp	Arg	Leu	Cys	Lys	Ile	Cys	Leu
1				5					10				15		
Gly	Ala	Glu	Lys	Thr	Val	Cys	Phe	Val	Pro	Cys	Gly	His	Val	Val	Ala
	20				25							30			
Cys	Gly	Lys	Cys	Ala	Ala	Gly	Val	Thr	Thr	Cys	Pro	Val	Cys		
	35					40						45			

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GAATTCCGGG AGACCTACAC CCCCGGAGAT CAGAGGTCA	TGCTGGCGTT CAGAGCCTAG	60
GAAGTGGCT GCGGTATCAG CCTAGCAGTA AAACCGACCA	GAAGCCATGC ACAAAACTAC	120
ATCCCCAGAG AAAGACTTGT CCCTTCCCCT CCCTGTCATC	TCACCATGAA CATGGTTCAA	180
GACAGCGCCT TTCTAGCCAA GCTGATGAAG AGTGCTGACA	CCTTTGAGTT GAAGTATGAC	240
TTTCCTGTG AGCTGTACCG ATTGTCCACG TATTCA	GCTT TTCCAGGGG AGTTCCCTGTG	300
TCAGAAAGGA GTCTGGCTCG TGCTGGCTTT TACTACACTG	GTGCCAATGA CAAGGTCAAG	360

0 1 2 3 4 5 6 7 8 9

TGCTTCTGCT	GTGGCCTGAT	GCTAGACAAC	TGGAAACAAG	GGGACAGTCC	CATGGAGAAG	420
CACAGAAAGT	TGTACCCCAG	CTGCAACTT	GTACAGACTT	TGAATCCAGC	CAACAGTCTG	480
GAAGCTAGTC	CTCGGCCCTTC	TCTTCCTTCC	ACGGCGATGA	GCACCATGCC	TTTGAGCTTT	540
GCAAGTTCTG	AGAATACTGG	CTATTTCACT	GGCTCTTACT	CGAGCTTCC	CTCAGACCC	600
GTGAACATTCC	GAGCAAATCA	AGATTGTCT	GCTTGAGCA	CAAGTCCCTA	CCACTTTGCA	660
ATGAACACAG	AGAAGGCCAG	ATTACTCAC	TATGAAACAT	GGCCATTGTC	TTTCTGTCA	720
CCAGCAAAGC	TGGCCAAAGC	AGGCTTCTAC	TACATAGGAC	CTGGAGATAG	AGTGGCCTGC	780
TTTGGTGGCG	ATGGGAAACT	GAGCAACTGG	GAACGTAAGG	ATGATGCTAT	GTCAGAGCAC	840
CAGAGGCATT	TCCCCAGCTG	TCCGTTCTTA	AAAGACTTGG	GTCAGTCTGC	TTCGAGATAC	900
ACTGTCTCTA	ACCTGAGCAT	GCAGACACAC	GCAGCCCGTA	TTAGAACATT	CTCTAACTGG	960
CCTTCTAGTG	CACTAGTTCA	TTCCCAGGAA	CTTGCAAGTG	CGGGCTTTA	TTATACAGGA	1020
CACAGTGATG	ATGTCAAGTG	TTTATGCTGT	GATGGTGGGC	TGAGGTGCTG	GGAATCTGGA	1080
GATGACCCCT	GGGTGGAACA	TGCCAAGTGG	TTTCCAAGGT	GTGAGTACTT	GCTCAGAACATC	1140
AAAGGCCAAG	AATTTGTCAG	CCAAGTTCAA	GCTGGCTATC	CTCATCTACT	TGAGCAGCTA	1200
TTATCTACGT	CAGACTCCCC	AGAAGATGAG	AATGCAGACG	CAGCAATCGT	GCATTTGGC	1260
CCTGGAGAAA	GTTCGGAAGA	TGTCGTATG	ATGAGCACGC	CTGTGGTTAA	AGCAGCCTTG	1320
GAAATGGGCT	TCAGTAGGAG	CCTGGTGAGA	CAGACGGTTC	AGTGGCAGAT	CCTGGCCACT	1380
GGTGAGAACT	ACAGGACCGT	CAGTGACCTC	GTTATAGGCT	TACTCGATGC	AGAAGACGAG	1440
ATGAGAGAGG	AGCAGATGGA	GCAGGCGGCC	GAGGAGGAGG	AGTCAGATGA	TCTAGCACTA	1500
ATCCGGAAGA	ACAAAATGGT	GCTTTCCAA	CATTGACGT	GTGTGACACC	AATGCTGTAT	1560
TGCCCTCTAA	GTGCAAGGGC	CATCACTGAA	CAGGAGTGCA	ATGCTGTGAA	ACAGAAACCA	1620
CACACCTTAC	AAGCAAGCAC	ACTGATTGAT	ACTGTGTTAG	CAAAAGGAAA	CACTGCAGCA	1680
ACCTCATTCA	GAAACTCCCT	TCGGAAATT	GACCCTGCGT	TATACAGAGA	TATATTGTG	1740
CAACAGGACA	TTAGGAGTCT	TCCCACAGAT	GACATTGCAG	CTCTACCAAT	GGAAGAACAG	1800
TTGGGGCCCC	TCCCCGGAGGA	CAGAATGTGT	AAAGTGTGTA	TGGACCGAGA	GGTATCCATC	1860
GTGTTCATTC	CCTGTGGCCA	TCTGGTCGTG	TGCAAAGACT	GCGCTCCCTC	TCTGAGGAAG	1920
TGTCCCATCT	GTAGAGGGAC	CATCAAGGGC	ACAGTGCACCA	CATTCTCTC	CTGAACAAAGA	1980
CTAATGGTCC	ATGGCTGCAA	CTTCAGCCAG	GAGGAAGTTC	ACTGTCACTC	CCAGTTCCAT	2040
TCGGAACCTG	AGGCCAGCCT	GGATAGCAG	AGACACCGCC	AAACACACAA	ATATAAACAT	2100
AAAAAACTTT	TGTCTGAAGT	CAAGAATGAA	TGAATTACTT	ATATAATAAT	TTTAATTGGT	2160
TTCCCTAAAAA	GTGCTATTTG	TTCCCAACTC	AGAAAATTGT	TTTCTGTAAA	CATATTTACA	2220

TACTACCTGC ATCTAAAGTA TTTCATATATT CATATATTCA GATGTCATGA GAGAGGGTTT	2280
TGTTCTTGTGTT CCTGAAAAGC TGGTTTATCA TCTGATCAGC ATATACTGCG CAACGGGCAG	2340
GGCTAGAACATC CATGAACCAA GCTGCAAAGA TCTCACGCTA AATAAGGCGG AAAGATTTGG	2400
—AGAAACGAAA—GGAAATTCTT—TCCTGTCCAA—TGTATACTCT—TCAGACTAAT—GACCTCTTCC—	2460
TATCAAGGCCT TCTA	2474

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 602 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met	Asn	Met	Val	Gln	Asp	Ser	Ala	Phe	Leu	Ala	Lys	Leu	Met	Lys	Ser
1				5					10				15		
Ala	Asp	Thr	Phe	Glu	Leu	Lys	Tyr	Asp	Phe	Ser	Cys	Glu	Leu	Tyr	Arg
						20			25				30		
Leu	Ser	Thr	Tyr	Ser	Ala	Phe	Pro	Arg	Gly	Val	Pro	Val	Ser	Glu	Arg
					35			40				45			
Ser	Leu	Ala	Arg	Ala	Gly	Phe	Tyr	Tyr	Thr	Gly	Ala	Asn	Asp	Lys	Val
						50		55				60			
Lys	Cys	Phe	Cys	Cys	Gly	Leu	Met	Leu	Asp	Asn	Trp	Lys	Gln	Gly	Asp
						65		70			75				80
Ser	Pro	Met	Glu	Lys	His	Arg	Lys	Leu	Tyr	Pro	Ser	Cys	Asn	Phe	Val
						85			90					95	
Gln	Thr	Leu	Asn	Pro	Ala	Asn	Ser	Leu	Glu	Ala	Ser	Pro	Arg	Pro	Ser
						100			105				110		
Leu	Pro	Ser	Thr	Ala	Met	Ser	Thr	Met	Pro	Leu	Ser	Phe	Ala	Ser	Ser
						115			120				125		
Glu	Asn	Thr	Gly	Tyr	Phe	Ser	Gly	Ser	Tyr	Ser	Ser	Phe	Pro	Ser	Asp
						130		135				140			
Pro	Val	Asn	Phe	Arg	Ala	Asn	Gln	Asp	Cys	Pro	Ala	Leu	Ser	Thr	Ser
						145		150			155			160	
Pro	Tyr	His	Phe	Ala	Met	Asn	Thr	Glu	Lys	Ala	Arg	Leu	Leu	Thr	Tyr
							165		170				175		
Glu	Thr	Trp	Pro	Leu	Ser	Phe	Leu	Ser	Pro	Ala	Lys	Leu	Ala	Lys	Ala
						180			185				190		
Gly	Phe	Tyr	Tyr	Ile	Gly	Pro	Gly	Asp	Arg	Val	Ala	Cys	Phe	Ala	Cys

195

200

205

Asp Gly Lys Leu Ser Asn Trp Glu Arg Lys Asp Asp Ala Met Ser Glu
 210 215 220

His Gln Arg His Phe Pro Ser Cys Pro Phe Leu Lys Asp Leu Gly Gln
 225 230 235 240

Ser Ala Ser Arg Tyr Thr Val Ser Asn Leu Ser Met Gln Thr His Ala
 245 250 255

Ala Arg Ile Arg Thr Phe Ser Asn Trp Pro Ser Ser Ala Leu Val His
 260 265 270

Ser Gln Glu Leu Ala Ser Ala Gly Phe Tyr Tyr Gly His Ser Asp
 275 280 285

Asp Val Lys Cys Leu Cys Cys Asp Gly Gly Leu Arg Cys Trp Glu Ser
 290 295 300

Gly Asp Asp Pro Trp Val Glu His Ala Lys Trp Phe Pro Arg Cys Glu
 305 310 315 320

Tyr Leu Leu Arg Ile Lys Gly Gln Glu Phe Val Ser Gln Val Gln Ala
 325 330 335

Gly Tyr Pro His Leu Leu Glu Gln Leu Leu Ser Thr Ser Asp Ser Pro
 340 345 350

Glu Asp Glu Asn Ala Asp Ala Ala Ile Val His Phe Gly Pro Gly Glu
 355 360 365

Ser Ser Glu Asp Val Val Met Met Ser Thr Pro Val Val Lys Ala Ala
 370 375 380

Leu Glu Met Gly Phe Ser Arg Ser Leu Val Arg Gln Thr Val Gln Trp
 385 390 395 400

Gln Ile Leu Ala Thr Gly Glu Asn Tyr Arg Thr Val Ser Asp Leu Val
 405 410 415

Ile Gly Leu Leu Asp Ala Glu Asp Glu Met Arg Glu Glu Gln Met Glu
 420 425 430

Gln Ala Ala Glu Glu Glu Ser Asp Asp Leu Ala Leu Ile Arg Lys
 435 440 445

Asn Lys Met Val Leu Phe Gln His Leu Thr Cys Val Thr Pro Met Leu
 450 455 460

Tyr Cys Leu Leu Ser Ala Arg Ala Ile Thr Glu Gln Glu Cys Asn Ala
 465 470 475 480

Val Lys Gln Lys Pro His Thr Leu Gln Ala Ser Thr Leu Ile Asp Thr
 485 490 495

Val Leu Ala Lys Gly Asn Thr Ala Ala Thr Ser Phe Arg Asn Ser Leu
 500 505 510

Arg Glu Ile Asp Pro Ala Leu Tyr Arg Asp Ile Phe Val Gln Gln Asp
 515 520 525

Ile Arg Ser Leu Pro Thr Asp Asp Ile Ala Ala Leu Pro Met Glu Glu
 530 535 540
 Gln Leu Arg Pro Leu Pro Glu Asp Arg Met Cys Lys Val Cys Met Asp
 545 550 555 560
 Arg Glu Val Ser Ile Val Phe Ile Pro Cys Gly His Leu Val Val Cys
 565 570 575
 Lys Asp Cys Ala Pro Ser Leu Arg Lys Cys Pro Ile Cys Arg Gly Thr
 580 585 590
 Ile Lys Gly Thr Val Arg Thr Phe Leu Ser
 595 600

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2416 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTGTGGTGGAA	GATCTATTGT	CCAAGTGGTG	AGAAAACCA	TCTGGAAGTT	TAAGCGGTCA	60
GAAATACTAT	TACTACTCAT	GGACAAAAC	GTCTCCCAGA	GACTCGCCCA	AGGTACCTTA	120
CACCCAAAAAA	CTTAAACGTA	TAATGGAGAA	GAGCACAAATC	TTGTCAAATT	GGACAAAGGA	180
GAGCGAAGAA	AAAATGAAGT	TTGACTTTTC	GTGTGAACTC	TACCGAATGT	CTACATATTC	240
AGCTTTCCC	AGGGGAGTTC	CTGTCTCAGA	GAGGAGTCTG	GCTCGTGTG	GCTTTATTAA	300
TACAGGTGTG	AATGACAAAG	TCAAGTGCTT	CTGCTGTGGC	CTGATGTTGG	ATAACTGGAA	360
ACAAGGGGAC	AGTCCTGTTG	AAAAGCACAG	ACAGTTCTAT	CCCAGCTGCA	GCTTTGTACA	420
GA	CTGCTT	TCAGCCAGTC	TGCAGTCTCC	ATCTAAGAAT	ATGTCTCCTG	480
TTTGACAT	TCGTCACCTC	TGGAACGAGG	TGGCATTAC	TCCAACCTGT	GCTCTAGCCC	540
TCTTAATTCT	AGAGCAGTGG	AAGACTTCTC	ATCAAGGATG	GATCCCTGCA	GCTATGCCAT	600
GAGTACAGAA	GAGGCCAGAT	TTCTTACTTA	CAGTATGTGG	CCTTTAAGTT	TTCTGTCACC	660
AGCAGAGCTG	GCCAGAGCTG	GCTTCTATTA	CATAGGGCCT	GGAGACAGGG	TGGCCTGTT	720
TGCCTGTGGT	GGGAAACTGA	GCAACTGGGA	ACCAAAGGAT	TATGCTATGT	CAGAGCACCC	780
CAGACATTTC	CCCCACTGTC	CATTTCTGGA	AAATACTTCA	GAAACACAGA	GGTTTAGTAT	840
ATCAAATCTA	AGTATGCAGA	CACACTCTGC	TCGATTGAGG	ACATTCTGT	ACTGGCCACC	900
TAGTGTTCCT	GTTCA	AGCAGCTTGC	AAGTGCTGGA	TTCTATTACG	TGGATCGCAA	960

TGATGATGTC AAGTGCCTTT GTTGTGATGG TGGCTTGAGA TGTTGGGAAC CTGGAGATGA 1020
CCCCTGGATA GAACACGCCA AATGGTTCC AAGGTGTGAG TTCTTGATAC GGATGAAGGG 1080
TCAGGAGTTT GTTGATGAGA TTCAAGCTAG ATATCCTCAT CTTCTTGAGC AGCTGTTGTC 1140
CACTTCAGAC ACCCCAGGAG AAGAAAATGC TGAGGCTACA GAGAGAGTGG TGCATTTGG 1200
CCCTGGAGAA AGTCGAAAG ATGTCGTCA GATGAGCACG CCTGTGGTTA AAGCAGCCTT 1260
GGAAATGGGC TTCAGTAGGA GCCTGGTGAG ACAGACGGTT CAGCGGCAGA TCCTGGCCAC 1320
TGGTGAGAAC TACAGGACCG TCAATGATAT TGTCTCAGTA CTTTGAAATG CTGAAGATGA 1380
GAGAAGAGAA GAGGAGAAGG AAAGACAGAC TGAAGAGATG GCATCAGGTG ACTTATCACT 1440
GATTCGGAAG AATAGAATGG CCCTCTTCA ACAGTTGACA CATGTCCTTC CTATCCTGGA 1500
TAATCTTCTT GAGGCCAGTG TAATTACAAA ACAGGAACAT GATATTATTA GACAGAAAAC 1560
ACAGATAACCC TTACAAGCAA GAGAGCTTAT TGACACCGTT TTAGTCAAGG GAAATGCTGC 1620
AGCCAACATC TTCAAAAAACT CTCTGAAGGG AATTGACTCC ACGTTATATG AAAACTTATT 1680
TGTGGAAAAG AATATGAAGT ATATTCCAAC AGAAGACGTT TCAGGCTTGT CATTGGAAGA 1740
GCAGTTGCGG AGATTACAAG AAGAACGAAC TTGCAAAGTG TGTATGGACA GAGAGGTTTC 1800
TATTGTGTTCA ATTCCGTGTG GTCATCTAGT AGTCTGCCAG GAATGTGCC CTTCTCTAAG 1860
GAAGTGCCCC ATCTGCAGGG GGACAATCAA GGGGACTGTG CGCACATTTC TCTCATGAGT 1920
GAAGAATGGT CTGAAAGTAT TGTTGGACAT CAGAAGCTGT CAGAACAAAG AATGAACATAC 1980
TGATTTCAGC TCTTCAGCAG GACATTCTAC TCTCTTCAA GATTAGTAAT CTTGCTTTAT 2040
GAAGGGTAGC ATTGTATATT TAAGCTTAGT CTGTTGCAAG GGAAGGTCTA TGCTGTTGAG 2100
CTACAGGACT GTGTCTGTT CAGAGCAGGA GTTGGGATGC TTGCTGTATG TCCTTCAGGA 2160
CTTCTGGGA TTTGGGAATT TGGGGAAAGC TTTGGAATCC AGTGATGTGG AGCTCAGAAA 2220
TCCTGGAACC AGTGACTCTG GTACTCAGTA GATAGGGTAC CCTGTACTTC TTGGTGCTTT 2280
TCCAGTCTGG GAAATAAGGA GGAATCTGCT GCTGGTAAAA ATTTGCTGGA TGTGAGAAAT 2340
AGATGAAAGT GTTCGGGTG GGGCGTGCA TCAGTGTAGT GTGTGCAGGG ATGTATGCAG 2400
GCCAAACACT GTGTAG 2416

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Glu Lys Ser Thr Ile Leu Ser Asn Trp Thr Lys Glu Ser Glu Glu
1 5 10 15

Lys Met Lys Phe Asp Phe Ser Cys Glu Leu Tyr Arg Met Ser Thr Tyr
20 25 30

Ser Ala Phe Pro Arg Gly Val Pro Val Ser Glu Arg Ser Leu Ala Arg
35 40 45

Ala Gly Phe Tyr Tyr Thr Gly Val Asn Asp Lys Val Lys Cys Phe Cys
50 55 60

Cys Gly Leu Met Leu Asp Asn Trp Lys Gln Gly Asp Ser Pro Val Glu
65 70 75 80

Lys His Arg Gln Phe Tyr Pro Ser Cys Ser Phe Val Gln Thr Leu Leu
85 90 95

Ser Ala Ser Leu Gln Ser Pro Ser Lys Asn Met Ser Pro Val Lys Ser
100 105 110

Arg Phe Ala His Ser Ser Pro Leu Glu Arg Gly Gly Ile His Ser Asn
115 120 125

Leu Cys Ser Ser Pro Leu Asn Ser Arg Ala Val Glu Asp Phe Ser Ser
130 135 140

Arg Met Asp Pro Cys Ser Tyr Ala Met Ser Thr Glu Glu Ala Arg Phe
145 150 155 160

Leu Thr Tyr Ser Met Trp Pro Leu Ser Phe Leu Ser Pro Ala Glu Leu
165 170 175

Ala Arg Ala Gly Phe Tyr Tyr Ile Gly Pro Gly Asp Arg Val Ala Cys
180 185 190

Phe Ala Cys Gly Gly Lys Leu Ser Asn Trp Glu Pro Lys Asp Tyr Ala
195 200 205

Met Ser Glu His Arg Arg His Phe Pro His Cys Pro Phe Leu Glu Asn
210 215 220

Thr Ser Glu Thr Gln Arg Phe Ser Ile Ser Asn Leu Ser Met Gln Thr
225 230 235 240

His Ser Ala Arg Leu Arg Thr Phe Leu Tyr Trp Pro Pro Ser Val Pro
245 250 255

Val Gln Pro Glu Gln Leu Ala Ser Ala Gly Phe Tyr Tyr Val Asp Arg
260 265 270

Asn Asp Asp Val Lys Cys Leu Cys Cys Asp Gly Gly Leu Arg Cys Trp
275 280 285

Glu Pro Gly Asp Asp Pro Trp Ile Glu His Ala Lys Trp Phe Pro Arg
290 295 300

Cys Glu Phe Leu Ile Arg Met Lys Gly Gln Glu Phe Val Asp Glu Ile
305 310 315 320

Gln Ala Arg Tyr Pro His Leu Leu Glu Gln Leu Leu Ser Thr Ser Asp
 325 330 335
 Thr Pro Gly Glu Glu Asn Ala Asp Pro Thr Glu Thr Val Val His Phe
 340 345 350
 Gly Pro Gly Glu Ser Ser Lys Asp Val Val Met Met Ser Thr Pro Val
 355 360 365
 Val Lys Ala Ala Leu Glu Met Gly Phe Ser Arg Ser Leu Val Arg Gln
 370 375 380
 Thr Val Gln Arg Gln Ile Leu Ala Thr Gly Glu Asn Tyr Arg Thr Val
 385 390 395 400
 Asn Asp Ile Val Ser Val Leu Leu Asn Ala Glu Asp Glu Arg Arg Glu
 405 410 415
 Glu Glu Lys Glu Arg Gln Thr Glu Glu Met Ala Ser Gly Asp Leu Ser
 420 425 430
 Leu Ile Arg Lys Asn Arg Met Ala Leu Phe Gln Gln Leu Thr His Val
 435 440 445
 Leu Pro Ile Leu Asp Asn Leu Leu Glu Ala Ser Val Ile Thr Lys Gln
 450 455 460
 Glu His Asp Ile Ile Arg Gln Lys Thr Gln Ile Pro Leu Gln Ala Arg
 465 470 475 480
 Glu Leu Ile Asp Thr Val Leu Val Lys Gly Asn Ala Ala Ala Asn Ile
 485 490 495
 Phe Lys Asn Ser Leu Lys Gly Ile Asp Ser Thr Leu Tyr Glu Asn Leu
 500 505 510
 Phe Val Glu Lys Asn Met Lys Tyr Ile Pro Thr Glu Asp Val Ser Gly
 515 520 525
 Leu Ser Leu Glu Glu Gln Leu Arg Arg Leu Gln Glu Glu Arg Thr Cys
 530 535 540
 Lys Val Cys Met Asp Arg Glu Val Ser Ile Val Phe Ile Pro Cys Gly
 545 550 555 560
 His Leu Val Val Cys Gln Glu Cys Ala Pro Ser Leu Arg Lys Cys Pro
 565 570 575
 Ile Cys Arg Gly Thr Ile Lys Gly Thr Val Arg Thr Phe Leu Ser
 580 585 590